

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 47.2765 Seconds  
(without alignments)  
1199.218 Million cell updates/sec

Title: US-10-724-274-1  
Perfect score: 657  
Sequence: 1 QVQLKESGFLVAPSSQSLI.....TTGDDALDWGQTSVTVSS 124

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8.\*  
1: Geneseq1980s.\*  
2: Geneseq1990s.\*  
3: Geneseq2000s.\*  
4: Geneseq2001s.\*  
5: Geneseq2002s.\*  
6: Geneseq2003as.\*  
7: Geneseq2003bs.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*  
10: Geneseq2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	657	100.0	124	8	Adt77619 IIA1 VH p
2	657	100.0	124	9	Aeb51138 Mouse ant
3	657	100.0	143	8	Adq31879 Antibody
4	657	100.0	143	8	Adq31905 Murine an
5	657	100.0	143	8	Adq31875 Antibody
6	657	100.0	143	8	Adt77638 Antibody
7	657	100.0	143	8	Adt77634 Antibody
8	657	100.0	143	9	Aeb51153 Chimeric
9	657	100.0	143	9	Aeb51180 Chimeric
10	657	100.0	143	9	Aed49294 Anti-alpha
11	657	100.0	143	9	Aed49290 Anti-alpha
12	657	100.0	232	8	Adq31887 Antibody
13	657	100.0	232	8	Adt77646 Chimeric
14	657	100.0	232	9	Aeb51165 Chimeric
15	657	100.0	451	8	Adq31884 Antibody
16	657	100.0	451	8	Adt51712 M200 anti
17	657	100.0	451	8	Adt51711 M200 anti
18	657	100.0	451	8	Adt51709 M200 anti
19	657	100.0	451	8	Adt51713 M200 anti
20	657	100.0	451	8	Adt51710 M200 anti
21	657	100.0	451	8	Adt77643 Antibody
22	657	100.0	451	9	Aeb51162 Chimeric
23	657	100.0	451	10	Aef12090 Anti-alpha

24	657	100.0	451	10	Aef16428	Chimeric
25	657	100.0	451	10	Aef16425	Chimeric
26	657	100.0	451	10	Aef16426	Chimeric
27	657	100.0	451	10	Aef16427	Chimeric
28	657	100.0	451	10	Aef16424	Chimeric
29	627	95.4	136	9	Aeb51157	Chimeric
30	568	86.5	124	8	Adq31861	Humanised
31	568	86.5	124	8	Adt77620	1 VH pept
32	568	86.5	124	9	Aeb51139	Humanized
33	559	85.1	124	8	Adq31865	Humanised
34	559	85.1	124	8	Adt77624	5 VH pept
35	559	85.1	124	9	Aeb51143	Humanised
36	550	83.7	124	8	Adq31864	Humanised
37	550	83.7	124	8	Adt77623	4 VH pept
38	550	83.7	124	9	Aeb51142	Humanized
39	549	83.6	124	8	Adq31862	Humanised
40	549	83.6	124	8	Adt77621	2 VH pept
41	549	83.6	124	9	Aeb51140	Humanized
42	539	82.0	451	8	Adq31890	Antibody
43	539	82.0	451	9	Aeb51168	Chimeric
44	536.5	81.7	119	10	Aef10439	Mouse mab
45	522	79.5	124	8	Adq31863	Humanised

ALIGNMENTS

RESULT 1  
ADT77619  
ID ADT77619 standard; peptide; 124 AA.

XX ADT77619;

DT 13-JAN-2005 (first entry)

XX IIA1 VH peptide.

DE heavy; chain; variable; region; light; constant; antibody;  
KW macrophage behaviour; wound site; eye; alphasbetal;  
KW integral binding agent; RPS cell; phagocytic activity; secretion;  
KW cytokine; chemokine; mediator; inflammatory response; granulation; burn;  
KW bone; cartilage; vascular; ligament; tendon; keloid formation; arthritis;  
KW scleroderma; tissue inflammation; rheumatoid arthritis;  
KW Wegener's Granulomatosis; Churg-Straus-allergic granulomatosis;  
KW eosinophilic granulomata; midline granuloma; demoid; sarcoidosis;  
KW macular degeneration; proliferative vitreoretinopathy;  
KW proliferative diabetic retinopathy; uterine fibroid;  
KW arteritis temporalis; Takayasu's arteritis; Crohn's disease;  
KW idiopathic pulmonary fibrosis; allergic pulmonary fibrosis;  
KW wound healing; scar formation.

XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..25 /label= FR1
Peptide	4..124 /label= FR4
Peptide	26..35 /label= CDR1
Peptide	36..49 /label= FR2
Peptide	50..65 /label= CDR2
Peptide	66..97 /label= FR3
Peptide	98..113 /label= CDR3

XX W02004089988-A2.

XX 21-OCT-2004.

XX

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 13.0696 Seconds  
(without alignments)  
830.460 Million cell updates/sec

Title: US-10-724-274-1

Perfect score: 657

Sequence: 1 QVQLKESGPGLVAPQSLSITCTISGFSLTDTGVHVRQPPGKGLVWLVIWDSGSTYN 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SID3S/ptodata/2/iaa/5 COMB.pcp.\*
- 2: /EMC\_Celerra\_SID3S/ptodata/2/iaa/6 COMB.pcp.\*
- 3: /EMC\_Celerra\_SID3S/ptodata/2/iaa/7 COMB.pcp.\*
- 4: /EMC\_Celerra\_SID3S/ptodata/2/iaa/H COMB.pcp.\*
- 5: /EMC\_Celerra\_SID3S/ptodata/2/iaa/PCTUS COMB.pcp.\*
- 6: /EMC\_Celerra\_SID3S/ptodata/2/iaa/RE COMB.pcp.\*
- 7: /EMC\_Celerra\_SID3S/ptodata/2/iaa/backfilese1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517.5	78.8	119	1	US-08-752-844-16
2	517.5	78.8	119	1	US-08-591-196-16
3	517.5	78.8	119	2	US-09-293-533-16
4	502	76.4	120	1	US-08-652-558-38
5	501.5	76.3	142	3	US-08-772-103-4
6	497	75.6	121	2	US-08-881-037-67
7	495.5	75.4	113	2	US-08-726-219A-218
8	495.5	75.4	113	2	US-08-196-522-218
9	492	74.9	140	2	US-08-943-136-4
10	492	74.9	140	2	US-08-973-518-4
11	490	74.6	116	2	US-09-232-290-36
12	490	74.6	135	2	US-10-351-748-31
13	489	74.4	239	1	US-08-860-174A-2
14	489	74.4	241	2	US-08-726-219A-187
15	489	74.4	241	2	US-09-196-522-187
16	489	74.4	272	2	US-09-726-219A-183
17	489	74.4	272	2	US-09-196-522-183
18	487.5	74.2	121	2	US-10-056-052A-12
19	486	74.0	116	2	US-10-194-975-100
20	486	74.0	137	1	US-08-621-751A-4
21	485.5	73.9	222	1	US-08-190-199A-67
22	485.5	73.9	235	1	US-08-190-199A-61
23	483.5	73.6	119	2	US-08-483-749A-14
24	481	73.2	112	2	US-09-189-129-3
25	481	73.2	112	2	US-09-824-286-3
26	479.5	73.0	152	1	US-08-752-844-16

27	479.5	73.0	152	1	US-08-591-196-4	Sequence 4, Appli
28	479.5	73.0	152	2	US-09-192-838B-4	Sequence 4, Appli
29	479.5	73.0	152	2	US-09-293-533-4	Sequence 4, Appli
30	479.5	73.0	152	2	US-09-324-191-4	Sequence 4, Appli
31	479.5	73.0	263	1	US-08-752-844-66	Sequence 66, Appl
32	479.5	73.0	263	2	US-09-293-533-66	Sequence 15, Appl
33	478.5	72.8	119	1	US-08-667-769A-15	Sequence 15, Appl
34	478.5	72.8	119	2	US-10-700-740-15	Sequence 15, Appl
35	478.5	72.8	119	5	PCT-US95-17082A-15	Patent No. 5455030
36	478.5	72.8	242	7	5455030-15	Sequence 24, Appl
37	477.5	72.7	115	2	US-10-056-052A-24	Sequence 13, Appl
38	477	72.6	241	2	US-09-554-765-13	Sequence 16, Appl
39	474	72.1	118	2	US-10-056-052A-16	Sequence 4, Appli
40	468	71.2	116	2	US-08-397-411-4	Sequence 41, Appli
41	468	71.2	122	2	US-09-232-290-41	Sequence 112, App
42	467	71.1	120	2	US-10-194-975-112	Sequence 12, Appl
43	466.5	71.0	107	1	US-08-122-546-12	Sequence 12, Appl
44	466.5	71.0	107	1	US-08-764-938-12	Sequence 12, Appl
45	466.5	71.0	107	2	US-09-131-052-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-08-752-844-16  
; Sequence 16, Application US/08752844  
; Patent No. 5935821  
; GENERAL INFORMATION:  
; APPLICANT: Chatterjee, Malaya  
; APPLICANT: Poon, Kenneth A.  
; APPLICANT: Chatterjee, Sunil K.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE  
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/752,844  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 30414-20002.21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-752-844-16

Query Match 78.8%; Score 517.5; DB 1; Length 119;  
Best Local Similarity 80.2%; Pred. No. 8.7e-42;  
Matches 101; Conservative 6; Mismatches 10; Indels 9; Gaps 2;

Qy 1 QVQLKESGPGLVAPQSLSITCTISGFSLTDTGVHVRQPPGKGLVWLVIWDSGSTYN 60

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 7.42225 Seconds  
(without alignments)  
1607.447 Million cell updates/sec

Title: US-10-724-274-1  
Perfect score: 657  
Sequence: 1 QVQLKESGPGLVAPQSLSI.....TTTGDALDYWGQTSVTSS 124

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	510	77.6	144	2	S11244	Ig gamma-2a chain
2	503	76.6	122	2	S20809	Ig heavy chain v r
3	500.5	76.2	144	1	G2MS14	Ig heavy chain pre
4	499	76.0	117	2	S38563	Ig heavy chain v r
5	492	74.9	141	2	S52446	Ig heavy chain v r
6	490	74.6	120	2	PL0087	Ig heavy chain v r
7	489	74.4	122	2	A49049	Ig heavy chain v r
8	488.5	74.4	140	2	S55028	Ig heavy chain v r
9	484.5	73.7	114	2	S11106	Ig heavy chain v r
10	478.5	72.8	112	2	S11100	Ig heavy chain v r
11	475.5	72.4	111	2	S26324	Ig heavy chain pre
12	473	72.0	139	2	A32456	Ig gamma-2b chain
13	472.5	71.9	231	2	PC4155	Ig heavy chain (an
14	470	71.5	112	2	S32786	Ig heavy chain v r
15	469.5	71.5	116	2	S11102	Ig gamma-1 chain p
16	469.5	71.5	140	2	S14238	Ig heavy chain v r
17	469.5	71.4	116	2	S42484	Ig heavy chain v r
18	469	71.3	110	2	S26323	Ig heavy chain v r
19	468.5	71.3	113	2	S11101	Ig heavy chain v r
20	467.5	71.2	113	2	S11103	Ig heavy chain v r
21	466	70.9	101	2	S03466	Ig gamma-2a chain
22	466	70.9	135	2	S31913	Ig heavy chain v r
23	465.5	70.9	118	2	PQ0266	Ig heavy chain v r
24	463.5	70.5	114	2	S11099	Ig heavy chain v r
25	463.5	70.5	127	2	B31807	Ig heavy chain v r
26	458.5	69.8	115	2	S11103	Ig heavy chain v r
27	457.5	69.6	106	2	S26322	Ig heavy chain v r
28	454.5	69.2	106	2	S14489	Ig heavy chain v r
29	452.5	68.9	121	2	D30560	Ig heavy chain v r

30 450.5 68.6 115 2 S11107  
31 447.5 68.1 109 2 S11109  
32 446 67.9 117 2 S10111  
33 444 67.6 107 2 S14492  
34 443 67.4 115 2 S26470  
35 440.5 67.0 112 2 S11098  
36 439.5 66.9 121 2 S31311  
37 438 66.7 107 2 S14491  
38 437 66.5 110 2 PH1024  
39 436 66.4 97 2 S55372  
40 435 66.2 107 2 S14493  
41 435 66.1 115 1 HVMS14  
42 434.5 66.1 100 2 S14490  
43 433.5 66.0 114 2 S11105  
44 433 65.9 98 2 S21812  
45 432.5 65.8 114 2 S26321

## ALIGNMENTS

## RESULT 1

S11244  
Ig gamma-2a chain precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S11244  
R:Wellman, A.A.; Meares, C.P., 1990  
Nucleic Acids Res. 18, 5281, 1990  
A:Title: Sequences of the Lym-1 antibody heavy and light chain variable regions.  
A:Reference number: S11244; MUID:90384832; PMID:2119497  
A:Accession: S11244  
A:Molecule type: mRNA  
A:Residues: 1-144 <WEL>  
A:Cross-references: UNIPARC:UPI0000176C81; EMBL:X53483  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
P:34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 510; DB 2; Length 144;  
Best Local Similarity 81.5%; Pred. No. 1.6e-38;  
Matches 101; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

Oy 1 QVQLKESGPGLVAPQSLSITCTISGFSLTSDYGVHVRQPPKGLVWLVWISDGSSTYN 60  
Db 20 QVQLKESGPGLVAPQSLSITCTISGFSLTSDYGVHVRQPPKGLVWLVWISDGSSTYN 79  
Oy 61 SALKSRMTIRKDNKSKSQVFLINSLQTDSDSAMYCARHGTYYGTTTGDALDYWGQTSV 120  
Db 80 SALKSRMTIRKDNKSKSQVFLINSLQTDSDSAMYCARHGTYYGTTTGDALDYWGQTSV 133

## RESULT 2

S20809  
Ig heavy chain V region (hybridoma C8) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S20809  
R:Hoogenboom, H.; Dubois, P.; Raus, J.; Volckaert, G.  
submitted to the EMBL Data Library, September 1990  
A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine ant  
A:Reference number: S20809  
A:Accession: S20809  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-122 <HOOG>  
A:Cross-references: UNIPARC:UPI000011588E; EMBL:X54692; NID:950249; PIDN:CAA38508.1; F  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Result No.	Score	Query Match	Length	DB	ID	Description	
1	500.5	76.2	144	1	HV43_MOUSE	P01819	mus musculus
2	499	76.0	484	2	Q5U472_MOUSE	Q5U472	mus musculus
3	483	73.5	482	2	Q91X92_MOUSE	Q91X92	mus musculus
4	481	73.2	121	2	Q99NG4_MOUSE	Q99NG4	mus musculus
5	470	71.5	591	2	Q5TOL9_RAT	Q5TOL9	rattus norv
6	456.5	69.5	469	2	Q5M839_RAT	Q5M839	rattus norv
7	444.5	67.7	477	2	Q510J1_RAT	Q510J1	rattus norv
8	435.5	66.3	458	2	Q5M842_RAT	Q5M842	rattus norv
9	436	66.2	115	1	HV44_MOUSE	P01820	mus musculus
10	406	61.8	116	1	HV45_MOUSE	P01821	mus musculus
11	379	57.7	485	2	Q561M5_MOUSE	Q561m5	mus musculus
12	376.5	57.3	487	2	Q58E53_MOUSE	Q58E53	mus musculus
13	373	56.8	135	1	HV02_XENLA	P20957	xenopus lae
14	373	56.8	483	2	Q5U413_MOUSE	Q5U413	mus musculus
15	367	55.9	560	2	Q4V801_XENLA	Q4V801	xenopus lae
16	367	55.9	573	2	Q8WU38_HUMAN	Q8WU38	homo sapien
17	364.5	55.5	485	2	Q59E54_MOUSE	Q59E54	mus musculus
18	363	55.3	617	2	Q569B3_RAT	Q569b3	rattus norv
19	357.5	54.4	476	2	Q6GMX1_HUMAN	Q6GMx1	homo sapien
20	354.5	54.0	119	2	Q9UL73_HUMAN	Q9UL73	homo sapien
21	352.5	53.7	121	1	HV3U_HUMAN	P01771	homo sapien
22	351	53.4	477	2	Q6GMXX7_HUMAN	Q6GMx7	homo sapien
23	350.5	53.3	240	2	Q65ZC9_HUMAN	Q65Zc9	homo sapien
24	350	53.3	118	2	Q811U5_MOUSE	Q811u5	mus musculus
25	350	53.3	478	2	Q5FVQ3_RAT	Q5Fvq3	rattus norv
26	349.5	53.2	472	2	Q6N089_HUMAN	Q6N089	homo sapien
27	349	53.1	465	2	Q6GMX6_HUMAN	Q6GMx6	homo sapien
28	349	53.1	469	2	Q569F4_HUMAN	Q569f4	homo sapien
29	346	52.7	126	1	HV3K_HUMAN	P01772	homo sapien
30	345.5	52.6	136	1	HV01_XENLA	P20956	xenopus lae
31	345.5	52.6	615	2	Q569B6_RAT	Q569b6	rattus norv

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 54.5205 Seconds  
(without alignments)  
1199.218 Million cell updates/sec

Title: US-10-724-274-16  
Perfect score: 752  
Sequence: 1 MAVGLLLCLVTFPSCVLSQ.....TTTGDAIDYMGQGTSTVSS 143

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*
- 10: Geneseq2006s.\*

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# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	100.0	143	8 ADQ31879	Adq31879 Antibody
2	752	100.0	143	8 ADQ31905	Adq31905 Murine an
3	752	100.0	143	8 ADQ31875	Adq31875 Antibody
4	752	100.0	143	8 ADT77638	Adt77638 Antibody
5	752	100.0	143	8 ADT77634	Adt77634 Antibody
6	752	100.0	143	9 AEB51153	Aeb51153 Chimeric
7	752	100.0	143	9 AEB51180	Aeb51180 Chimeric
8	752	100.0	143	9 AED49294	Aed49294 Anti-alph
9	752	100.0	143	9 AED49290	Aed49290 Anti-alph
10	722	96.0	136	9 AEB51157	Aeb51157 Chimeric
11	657	87.4	124	9 AEB51138	Aeb51138 Mouse ant
12	657	87.4	124	9 AEB51138	Adt77619 Antibody
13	657	87.4	232	8 ADQ31887	Adt77646 Antibody
14	657	87.4	232	8 ADQ31884	Aeb51165 Chimeric
15	657	87.4	232	9 AEB51165	Adq31884 Antibody
16	657	87.4	451	8 ADQ31884	Adt51712 M200 anti
17	657	87.4	451	8 ADT51711	Adt51711 M200 anti
18	657	87.4	451	8 ADT51709	Adt51709 M200 anti
19	657	87.4	451	8 ADT51713	Adt51713 M200 anti
20	657	87.4	451	8 ADT51710	Adt51710 M200 anti
21	657	87.4	451	8 ADT77643	Adt77643 Antibody
22	657	87.4	451	8 ADT77643	Aeb51162 Chimeric
23	657	87.4	451	9 AEB51162	

24	657	87.4	451	10 AEF12090	Aef12090 Anti-alph
25	657	87.4	451	10 AEF16428	Aef16428 Chimeric
26	657	87.4	451	10 AEF16425	Aef16425 Chimeric
27	657	87.4	451	10 AEF16426	Aef16426 Chimeric
28	657	87.4	451	10 AEF16427	Aef16427 Chimeric
29	657	87.4	451	10 AEF16424	Aef16424 Chimeric
30	581.5	77.3	183	2 AAR15326	Aar15326 IL-2 chim
31	581.5	77.3	183	2 AAR32128	Aar32128 Anti-IL2R
32	580.5	77.2	138	2 AAW01146	Aaw01146 MAb 10.1
33	575.5	76.5	358	5 AAE27929	Aae27929 Human CH2
34	575.5	76.5	358	5 ABB82838	Abb82838 Antibody
35	575.5	76.5	468	5 AAE27928	Aae27928 Human CSE
36	575.5	76.5	468	6 ABB82837	Abb82837 Antibody
37	574	76.3	135	1 AAP70991	Aap70991 Sequence
38	572.5	76.1	142	4 AAG66520	Aag66520 Mouse ant
39	571	75.9	137	2 AAW30277	Aaw30277 Heavy cha
40	570.5	75.9	152	2 AAY49210	Aay49210 MAB 1A7 h
41	570.5	75.9	152	2 AAY28469	Aay28469 Heavy cha
42	570.5	75.9	152	2 AAY21546	Aay21546 Monoclonal
43	570.5	75.9	152	6 ADA14770	Ada14770 Mouse ant
44	570.5	75.9	152	7 ADC35312	Adc35312 Monoclonal
45	570.5	75.9	152	10 AEF10365	Aef10365 Mouse mAb

## ALIGNMENTS

### RESULT 1

ADQ31879  
ADQ31879 standard; protein; 143 AA.

XX AC ADQ31879;  
XX XX 23-SEP-2004 (first entry)  
XX DE Antibody M200 VH amino acid sequence SEQ ID NO:20.

XX KW chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;  
XX KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;  
XX XX vascularisation; antiangiogenic; integrin alpha5beta5 antagonist.

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

XX WO2004056308-A2.

XX PD 08-JUL-2004.

XX PF 26-NOV-2003; 2003WO-US038172.

XX PR 26-NOV-2002; 2002US-0429743P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Ramakrishnan V, Powers D, Johnson DE, Jeffry U;

XX DR WPI; 2004-525316/50.

XX N-P8DB; ADQ31878.

XX PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling  
PT vascularization in injured tissue.

XX PS Claim 23; SEQ ID NO 20; 89pp; English.

XX CC The present invention describes a chimeric anti-alpha5beta-1 integrin  
XX CC antibody (I), comprising: (a) a first polypeptide sequence from a first  
XX CC source comprising one or more amino acid sequences selected from SEQ ID  
XX CC NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second  
XX CC polypeptide from a second source comprising a constant region sequence of  
XX CC an antibody of the second source, where the first and second polypeptide  
XX CC sequences form a protein complex that is immunoreactive with alpha5beta1  
XX CC integrin. Also described: (i) purifying (M1) pH-sensitive (I) comprises

GnCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 15.0722 Seconds  
(without alignments)  
830.460 Million cell updates/sec

Title: US-10-724-274-16

Perfect score: 752

Sequence: 1 MAVLGLLCLVTPFPSCVLSQ.....TTTGDDALDYWGQTSVTSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pdp.\*
- 2: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pdp.\*
- 3: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pdp.\*
- 4: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/8\_COMB.pdp.\*
- 5: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/9\_COMB.pdp.\*
- 6: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/10\_COMB.pdp.\*
- 7: /BMC\_Celerra\_SIDS3/ptodata/2/iaa/11\_COMB.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	76.3	135	2	US-10-351-748-31
2	572.5	76.1	142	3	US-09-772-103-4
3	571	75.9	137	1	US-08-621-751A-4
4	570.5	75.9	152	1	US-08-752-844-4
5	570.5	75.9	152	1	US-08-591-196-4
6	570.5	75.9	152	2	US-09-192-838B-4
7	570.5	75.9	152	2	US-09-293-533-4
8	570.5	75.9	152	2	US-09-324-191-4
9	570.5	75.9	263	1	US-08-752-844-66
10	570.5	75.9	263	2	US-09-533-66
11	552.5	73.5	478	2	US-09-770-916-2
12	542.5	72.1	138	1	US-07-634-278-33
13	542.5	72.1	138	1	US-08-477-728-33
14	542.5	72.1	138	1	US-08-474-040-33
15	542.5	72.1	138	1	US-08-487-200-33
16	542.5	72.1	138	2	US-08-484-537-33
17	542.5	72.1	138	3	US-09-718-998-33
18	541.5	72.0	140	2	US-08-943-136-4
19	541.5	72.0	140	2	US-08-973-518-4
20	522.5	69.5	142	3	US-09-772-103-10
21	517.5	68.8	119	1	US-08-752-844-16
22	517.5	68.8	119	1	US-08-591-196-16
23	517.5	68.8	119	2	US-09-293-533-16
24	517	68.8	137	1	US-08-621-751A-8
25	502	66.8	120	1	US-08-652-558-38
26	500.5	66.6	241	2	US-09-726-219A-187

Sequence 187, App  
Sequence 183, App  
Sequence 183, App  
Sequence 67, Appl  
Sequence 218, App  
Sequence 218, App  
Sequence 2, Appl  
Sequence 36, Appl  
Sequence 12, Appl  
Sequence 100, App  
Sequence 67, Appl  
Sequence 14, Appl  
Sequence 61, Appl  
Sequence 61, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 13, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 15, Appl

27 500.5 66.6 241 2 US-09-196-522-187  
28 500.5 66.6 272 2 US-09-726-219A-183  
29 500.5 66.6 272 2 US-09-196-522-183  
30 497 66.1 121 2 US-08-881-037-67  
31 495.5 65.9 113 2 US-09-726-219A-218  
32 495.5 65.9 113 2 US-09-196-522-218  
33 493 65.6 239 1 US-08-860-174A-2  
34 490 65.2 116 2 US-09-232-290-36  
35 487.5 64.8 121 2 US-10-056-052A-12  
36 486 64.6 116 2 US-10-194-975-100  
37 485.5 64.6 222 1 US-08-190-199A-67  
38 485.5 64.6 235 1 US-08-483-749A-14  
39 483.5 64.3 119 2 US-09-189-129-3  
40 481 64.0 112 2 US-09-824-286-3  
41 481 64.0 112 2 US-09-554-765-13  
42 481 64.0 241 2 US-08-667-769A-15  
43 478.5 63.6 119 1 US-10-700-740-15  
44 478.5 63.6 119 2 US-10-700-740-15  
45 478.5 63.6 119 5 PCT-US95-17082A-15

#### ALIGNMENTS

#### RESULT 1

US-10-351-748-31  
; Sequence 31, Application US/10351748  
; Patent No. 6982321

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul  
TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED  
FILE REFERENCE: 7806-011-999 (CAM 107814-999010)

CURRENT FILING DATE: 2003-01-24

PRIOR APPLICATION NUMBER: 08/452,462

PRIOR FILING DATE: 1995-05-26

PRIOR APPLICATION NUMBER: 07/942,146

PRIOR FILING DATE: 1992-09-08

PRIOR APPLICATION NUMBER: 07/624,515

PRIOR FILING DATE: 1990-12-07

PRIOR APPLICATION NUMBER: 07/189,814

PRIOR FILING DATE: 1988-05-03

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 31

LENGTH: 135

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Amino acid sequence of the variable domain gene of

OTHER INFORMATION: antibody D1.3 (Fig 7)

US-10-351-748-31

Query Match 76.3%; Score 574; DB 2; Length 135;  
Best Local Similarity 76.9%; Pred. No. 1.2e-48;  
Matches 110; Conservative 11; Mismatches 14; Indels 8; Gaps 1;

1 MAVLGLLCLVTPFPSCVLSQVLKESGPGVLVAPSQSLSTCTTSGFSLTDYGVHVRQPP 60

1 MAVLALLCLVTPFPSCVLSQVLKESGPGVLVAPSQSLSTCTTSGFSLTDYGVHVRQPP 60

61 GKGLWLVVWSDGSSTYNSALKSRMTIRKNSKSOVFLIMNSLOTTDDSSAMYTCARIGTY 120

61 GKGLWLVWSDGSSTYNSALKSRMTIRKNSKSOVFLIMNSLOTTDDSSAMYTCARIGTY 120

121 YGTTTGDALDYWGQTSVTSS 143

121 -----RLDYWGQTSVTSS 135

RESULT 2

US-09-772-103-4

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 8.55953 Seconds  
(without alignments)  
1607.447 Million cell updates/sec

Title: US-10-724-274-16  
Perfect score: 752  
Sequence: 1 MAVLGILLCLVTPPSCVLSQ.....TTTGDALDYWGQTSVTSS 143

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\* ;  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	80.5	144	2 S11244	Ig gamma-2a chain
2	580.5	77.2	144	1 G2MS14	Ig heavy chain pre
3	569	75.7	141	2 S52446	Ig heavy chain v r
4	565.5	75.2	140	2 S55028	Ig heavy chain v r
5	557	74.1	135	2 S31913	Ig gamma-2A chain
6	550	73.1	139	2 A32456	Ig heavy chain pre
7	529.5	70.4	140	2 S14238	Ig gamma-1 chain p
8	523	69.5	117	2 S10111	Ig heavy chain v r
9	519	69.0	115	1 HVMS14	Ig heavy chain pre
10	503	66.9	122	2 S20809	Ig heavy chain v r
11	499	66.4	117	2 S38563	Ig heavy chain v r
12	497	66.1	116	1 G1MS10	Ig heavy chain pre
13	496	66.0	116	2 A33932	Ig mu chain precu
14	490	65.2	120	2 PL0087	Ig heavy chain v r
15	489	65.0	122	2 A49049	Ig heavy chain v r
16	484.5	64.4	114	2 S11106	Ig heavy chain v r
17	478.5	63.6	112	2 S11100	Ig heavy chain v r
18	477	63.4	101	2 S03466	Ig heavy chain v r
19	475.5	63.2	111	2 S26324	Ig heavy chain v r
20	472.5	62.8	231	2 PC4155	Ig gamma-2b chain
21	470	62.5	118	2 S32786	Ig heavy chain (an
22	469.5	62.4	112	2 S11108	Ig heavy chain v r
23	469.5	62.4	116	2 S42484	Ig heavy chain v r
24	469	62.4	116	2 S26323	Ig heavy chain v r
25	468.5	62.3	110	2 S26323	Ig heavy chain v r
26	467.5	62.2	113	2 S11101	Ig heavy chain v r
27	465.5	61.9	118	2 PQ0266	Ig heavy chain v r
28	463.5	61.6	114	2 S11099	Ig heavy chain v r
29	463.5	61.6	127	2 B31807	Ig heavy chain v r

ALIGNMENTS

RESULT 1

S11244  
Ig gamma-2a chain precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C:Accession: S11244  
R:Wellman, A.A.; Mearns, C.F.  
Nucleic Acids Res. 18, 5281, 1990  
A:Title: Sequences of the Lym-1 antibody heavy and light chain variable regions.  
A:Reference number: S11244; MUID:90384832; PMID:2119497  
A:Accession: S11244  
A:Molecule type: mRNA  
A:Residues: 1-144 <WEL>  
A:Cross-references: UNIPARC:UPI0000176C81; EMBL:X53483  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 605; DB 2; Length 144;  
Best Local Similarity 83.9%; Pred. No. 5.7e-45;  
Matches 120; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

Qy	1	MAVLGILLCLVTPPSCVLSQVQLKESGPGLVAPQSISITCTISGFSITDYGVHVRQPP	60
Db	1	MAVLGILLCLVTPPSCVLSQVQLKESGPGLVAPQSISITCTISGFSITDYGVHVRQPP	60
Qy	61	GKGLWLVWISDGSSTYNSALKSRMTIRKDNKSQVFLIMNSIQTDSDAMYCARHCTY	120
Db	61	GKGLWLVWISDGSSTYNSALKSRMTIRKDNKSQVFLIMNSIQTDSDAMYCARHCTY	117
Qy	121	YGWTTTGDALDYWGQTSVTSS	143
Db	118	YGSTL---AFASWGHGTLVTSA	137

RESULT 2

G2MS14

Ig heavy chain precursor V region (MOPC 141) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Oct-1980 #sequence\_revision 31-Oct-1980 #text\_change 09-Jul-2004

C:Accession: A02094

R:Sakano, H.; Maki, R.; Kurosawa, Y.; Roeder, W.; Tonegawa, S.

Nature 286, 676-683, 1980

A:Title: Two types of somatic recombination are necessary for the generation of complex antibody repertoires.  
A:Reference number: A93229; MUID:81012133; PMID:6774258

A:Accession: A02094

A:Molecule type: DNA

A:Residues: 1-144 <SAK>

A:Cross-references: UNIPROT:P01819; UNIPARC:UPI000002726A; GB:V00768; GB:J00491; NID:G

A>Note: The sequence shown was determined from a differentiated gene isolated from a m

A>Note: The authors translated the codon TAT for residue 51 as Thr and TTA for residue

C:Genetics:

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:25 ; Search time 66.1503 Seconds  
(without alignments)  
1999.647 Million cell updates/sec

Title: US-10-724-274-16

Perfect score: 752  
Sequence: 1 MAVIGLLLCVLPFPSCVLSQ.....TTTGDDALDYWGQGTSTVTVSS 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	594	79.0	484	Q5U472_MOUSE	Q5U472 mus musculus
2	580.5	77.2	144	HV43_MOUSE	P01819 mus musculus
3	568	75.5	482	Q91X92_MOUSE	Q91X92 mus musculus
4	548	72.9	591	Q5I019_RAT	Q5I019 rattus norv
5	537.5	71.5	469	Q5M839_RAT	Q5M839 rattus norv
6	529.5	70.4	477	Q5I011_RAT	Q5I011 rattus norv
7	521.5	69.3	458	Q5M842_RAT	Q5M842 rattus norv
8	519	69.0	115	HV44_MOUSE	P01820 mus musculus
9	497	66.1	116	HV45_MOUSE	P01821 mus musculus
10	481	64.0	121	Q99NG4_MOUSE	Q99NG4 mus musculus
11	400	53.2	485	Q561M5_MOUSE	Q561M5 mus musculus
12	399.5	53.1	483	Q5U413_MOUSE	Q5U413 mus musculus
13	398.5	53.0	135	HV02_XENLA	P20957 xenopus lae
14	397.5	52.9	487	Q58E53_MOUSE	Q58E53 mus musculus
15	395.5	52.6	560	Q4V801_XENLA	Q4V801 xenopus lae
16	385.5	51.3	476	Q6GMX1_HUMAN	Q6GMX1 homo sapien
17	385.5	51.3	485	Q58E54_MOUSE	Q58E54 mus musculus
18	384	51.1	617	Q569B3_RAT	Q569B3 rattus norv
19	379	50.4	477	Q6GMX7_HUMAN	Q6GMX7 homo sapien
20	377	50.1	465	Q6GMX6_HUMAN	Q6GMX6 homo sapien
21	377	50.1	615	Q569B6_RAT	Q569B6 rattus norv
22	373.5	49.7	136	HV01_XENLA	P20956 xenopus lae
23	372	49.5	496	Q56KX8_HUMAN	Q56KX8 homo sapien
24	371.5	49.4	136	Q6LRQ5_MOUSE	Q6LRQ5 mus musculus
25	371.5	49.4	573	Q8WU38_HUMAN	Q8WU38 homo sapien
26	368.5	49.0	493	Q569J1_HUMAN	Q569J1 homo sapien
27	368	48.9	576	Q5P418_HUMAN	Q5P418 homo sapien
28	368	48.9	620	Q56EY0_HUMAN	Q56EY0 homo sapien
29	366	48.7	137	HV46_MOUSE	P01822 mus musculus
30	365	48.5	482	Q5VLR6_RAT	Q5VLR6 rattus norv
31	361	48.0	478	Q7Z379_HUMAN	Q7Z379 homo sapien

Q3B8R4 rattus norv  
Q5FVQ3 rattus norv  
Q99M22 mus musculus  
Q95973 homo sapien  
Q4VBH1 rattus norv  
Q569B8 rattus norv  
Q5UL73 homo sapien  
Q6N089 homo sapien  
P01771 homo sapien  
Q569F4 homo sapien  
Q65ZC9 homo sapien  
Q811U5 mus musculus  
Q6PDB8 mus musculus  
P01793 mus musculus

32 360.5 47.9 595 2 Q3B8R4\_RAT  
33 356 47.3 478 2 Q5FVQ3\_RAT  
34 356 47.3 479 2 Q99M22\_MOUSE  
35 355 47.2 150 2 Q95973\_HUMAN  
36 355 47.2 467 2 Q4VBH1\_RAT  
37 355 47.2 590 2 Q569B8\_RAT  
38 354.5 47.1 119 2 Q5UL73\_HUMAN  
39 354 47.1 472 2 Q6N089\_HUMAN  
40 352.5 46.9 121 1 HV3U\_HUMAN  
41 352 46.8 469 2 Q569F4\_HUMAN  
42 350.5 46.6 240 2 Q65ZC9\_MOUSE  
43 350 46.5 118 2 Q811U5\_MOUSE  
44 347.5 46.2 485 2 Q6PDB8\_MOUSE  
45 347 46.1 136 1 HV16\_MOUSE

#### ALIGNMENTS

#### RESULT 1

Q5U472\_MOUSE  
ID Q5U472\_MOUSE PRELIMINARY; PRT; 484 AA.  
AC Q5U472;  
DT 07-DEC-2004, integrated into UniprotKB/TREMBL.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE LOC544903 protein.  
GN Name=LOC544903;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT \*Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.\*;  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]

#### NUCLEOTIDE SEQUENCE

STRAIN=FVB/N; TISSUE=Colon; -

NIH MGC Project;

Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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EMBL; BC085241; AAH85241.1; -; mRNA.

Ensembl; ENSMUSG000000054328; Mus musculus.

InterPro; IPR003599; IG.

InterPro; IPR007110; IG-like.

InterPro; IPR003597; IG cl.

InterPro; IPR003006; IG\_MHC.

InterPro; IPR003596; IG\_v.



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 51.8517 Seconds  
(without alignments)  
1199.218 Million cell updates/sec

Title: US-10-724-274-20

Perfect score: 722

Sequence: 1 MAVGLGLLCLVTFPPSCVLSQ.....HGTYGVTGTDALDYWGQG 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	136	9 AEB51157	Aeb51157 Chimeric
2	722	100.0	143	8 ADQ31879	Adq31879 Antibody
3	722	100.0	143	8 ADQ31905	Adq31905 Murine an
4	722	100.0	143	8 ADQ31875	Adq31875 Antibody
5	722	100.0	143	8 ADT77638	Adt77638 Antibody
6	722	100.0	143	8 ADT77634	Adt77634 Antibody
7	722	100.0	143	9 AEB51153	Aeb51153 Chimeric
8	722	100.0	143	9 AEB51180	Aeb51180 Chimeric
9	722	100.0	143	9 AED49294	Aed49294 Anti-alpha
10	722	100.0	143	9 AED49290	Aed49290 Anti-alpha
11	627	86.8	124	8 ADT77619	Adt77619 IIAL VH p
12	627	86.8	124	9 AEB51138	Aeb51138 Mouse ant
13	627	86.8	232	8 ADQ31887	Adq31887 Antibody
14	627	86.8	232	8 ADT77646	Adt77646 Antibody
15	627	86.8	232	9 AEB51165	Aeb51165 Chimeric
16	627	86.8	451	8 AEB51184	Adq31884 Antibody
17	627	86.8	451	8 ADT51712	Adt51712 M200 anti
18	627	86.8	451	8 ADT51711	Adt51711 M200 anti
19	627	86.8	451	8 ADT51709	Adt51709 M200 anti
20	627	86.8	451	8 ADT51713	Adt51713 M200 anti
21	627	86.8	451	8 ADT51710	Adt51710 M200 anti
22	627	86.8	451	8 ADT77643	Adt77643 Antibody
23	627	86.8	451	9 AEB51162	Aeb51162 Chimeric

24	627	86.8	451	10 AEF12090	Aef12090 Anti-alpha
25	627	86.8	451	10 AEF16428	Aef16428 Chimeric
26	627	86.8	451	10 AEF16425	Aef16425 Chimeric
27	627	86.8	451	10 AEF16426	Aef16426 Chimeric
28	627	86.8	451	10 AEF16427	Aef16427 Chimeric
29	627	86.8	451	10 AEF16424	Aef16424 Chimeric
30	560.5	77.6	183	2 AAR15326	Aar15326 IL-2 chim
31	560.5	77.6	183	2 AAR32128	Aar32128 Anti-IL2R
32	551.5	76.4	358	5 AAE27929	Aae27929 Human CH2
33	551.5	76.4	358	6 ABB28838	Abb28838 Antibody
34	551.5	76.4	468	5 AAE27928	Aae27928 Human C5E
35	551.5	76.4	468	6 ABB28837	Abb28837 Antibody
36	550.5	76.2	138	2 AAW01146	Aaw01146 MAB 10.1
37	550	76.2	135	1 AAP70991	Aap70991 Sequence
38	548.5	76.0	142	4 AAG65520	Aag65520 Mouse ant
39	547	75.8	137	2 AAW30277	Aaw30277 Heavy cha
40	544	75.3	124	8 ADQ31861	Adq31861 Humanized
41	544	75.3	124	8 ADT77620	Adt77620 1 VH pept
42	544	75.3	124	9 AEB51139	Aeb51139 Humanized
43	540.5	74.9	152	2 AAY49210	Aay49210 MAB 1A7 h
44	540.5	74.9	152	2 AAY28469	Aay28469 Heavy cha
45	540.5	74.9	152	2 AAY21546	Aay21546 Monoclonal

#### ALIGNMENTS

RESULT 1

AEB51157

ID AEB51157 standard; protein; 136 AA.

XX AEB51157;

XX AEB51157;

DT 06-OCT-2005 (first entry)

XX Chimeric alpha-5/beta-1 integrin antibody M200 VH domain.

XX Integrin alpha-5/beta-1; chimeric antibody; antibody engineering;  
XX angiogenesis disorder; ocular disease; ophthalmological; antidiabetic;  
XX antiangiogenic; cardiovascular disease; macular degeneration;  
XX diabetic retinopathy; retinal neovascularization; vascularization.

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX US2005163769-A1.

XX 28-JUL-2005.

XX 23-APR-2004; 2004US-00830956.

XX 26-NOV-2002; 2002US-0429743P.

XX 30-SEP-2003; 2003US-0508149P.

XX 26-NOV-2003; 2003US-00724274.

XX (RAMA/) RAMAKRISHNAN V.

XX (POWE/) POWERS D.

XX (JOHN/) JOHNSON D E.

XX (JEFF/) JEFFERY U.

XX Ramakrishnan V, Powers D, Johnson DE, Jeffery U;

XX WPI; 2005-521374/53.

XX N-PSDB; AEB51156.

XX New chimeric anti-alpha5beta1 integrin antibody alpha-5/beta-1, useful for  
XX treating angiogenesis-associated ocular disease, ocular disease, or a  
XX growth factor-associated ocular disease.

XX Claim 1; SEQ ID NO 20; 69pp; English.

XX The invention relates to a novel chimeric anti-alpha-5/beta-1 integrin

CC

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 14.3344 Seconds  
(without alignments)  
830.460 Million cell updates/sec

Title: US-10-724-274-20

Perfect score: 722  
Sequence: 1 MAVGLLLCLVTPSCVLSQ.....HGTYGWTGTDALDYWGQ 136

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /EMC\_Celerra\_SID33/ptodata/2/iaa/5 COMB.pcp.\*  
2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6 COMB.pcp.\*  
3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7 COMB.pcp.\*  
4: /EMC\_Celerra\_SID33/ptodata/2/iaa/H COMB.pcp.\*  
5: /EMC\_Celerra\_SID33/ptodata/2/iaa/PCTUS COMB.pcp.\*  
6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE COMB.pcp.\*  
7: /EMC\_Celerra\_SID33/ptodata/2/iaa/backfile01.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	550	76.2	135	US-10-351-748-31	Sequence 31, Appl
2	548.5	76.0	142	US-09-772-103-4	Sequence 4, Appl
3	547	75.8	137	US-08-621-751A-4	Sequence 4, Appl
4	540.5	74.9	152	US-08-752-844-4	Sequence 4, Appl
5	540.5	74.9	152	US-08-591-196-4	Sequence 4, Appl
6	540.5	74.9	152	US-09-192-838B-4	Sequence 4, Appl
7	540.5	74.9	152	US-09-293-533-4	Sequence 4, Appl
8	540.5	74.9	152	US-09-324-131-4	Sequence 4, Appl
9	540.5	74.9	263	US-08-752-844-66	Sequence 66, Appl
10	540.5	74.9	263	US-09-293-533-66	Sequence 66, Appl
11	523.5	72.4	478	US-07-770-916-2	Sequence 2, Appl
12	521.5	72.2	138	US-07-634-278-33	Sequence 33, Appl
13	521.5	72.2	138	US-08-477-728-33	Sequence 33, Appl
14	521.5	72.2	138	US-08-474-040-33	Sequence 33, Appl
15	521.5	72.2	138	US-08-487-200-33	Sequence 33, Appl
16	521.5	72.2	138	US-08-484-537-33	Sequence 33, Appl
17	521.5	72.2	138	US-07-718-998-33	Sequence 33, Appl
18	515.5	71.4	140	US-08-943-136-4	Sequence 4, Appl
19	515.5	71.4	140	US-08-973-518-4	Sequence 4, Appl
20	498.5	69.0	142	US-09-772-103-10	Sequence 10, Appl
21	493	68.3	137	US-08-621-751A-8	Sequence 8, Appl
22	487.5	67.5	119	US-08-752-844-16	Sequence 16, Appl
23	487.5	67.5	119	US-08-591-196-16	Sequence 16, Appl
24	487.5	67.5	119	US-09-293-533-16	Sequence 16, Appl
25	473.5	65.6	241	US-09-726-219A-187	Sequence 187, App
26	473.5	65.6	241	US-09-196-522-187	Sequence 187, App

27 473.5 65.6 272 2 US-09-726-219A-183 Sequence 183, App  
28 473.5 65.6 272 2 US-09-196-522-183 Sequence 183, App  
29 472 65.4 120 1 US-08-652-558-38 Sequence 38, Appl  
30 471 65.2 121 2 US-08-881-037-67 Sequence 67, Appl  
31 468.5 64.9 113 2 US-09-726-219A-218 Sequence 218, App  
32 468.5 64.9 113 2 US-09-196-522-218 Sequence 12, App  
33 466.5 64.6 107 1 US-08-122-546-12 Sequence 12, Appl  
34 466.5 64.6 107 1 US-08-764-938-12 Sequence 12, Appl  
35 466.5 64.6 107 2 US-09-131-052-12 Sequence 12, Appl  
36 466.5 64.6 107 2 US-09-131-053A-12 Sequence 12, Appl  
37 466.5 64.6 121 2 US-10-056-052A-12 Sequence 3, Appl  
38 466 64.5 112 2 US-09-189-129-3 Sequence 3, Appl  
39 466 64.5 112 2 US-09-824-286-3 Sequence 36, Appl  
40 466 64.5 116 2 US-09-232-290-36 Sequence 2, Appl  
41 466 64.5 239 1 US-08-860-174A-2 Sequence 67, Appl  
42 464.5 64.3 222 1 US-08-190-199A-67 Sequence 61, Appl  
43 464.5 64.3 235 1 US-08-190-199A-61 Sequence 100, App  
44 462 64.0 116 2 US-10-194-975-100 Sequence 14, Appl  
45 455 63.0 107 1 US-07-942-245-14 Sequence 14, Appl

## ALIGNMENTS

## RESULT 1

US-10-351-748-31

; Sequence 31, Application US/10351748

; Patent No. 6982321

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 7806-011-999 (CAM 107814-999010)

; CURRENT APPLICATION NUMBER: US/10/351,748

; PRIOR FILING DATE: 2003-01-24

; PRIOR APPLICATION NUMBER: 08/452,462

; PRIOR FILING DATE: 1995-05-26

; PRIOR APPLICATION NUMBER: 07/942,146

; PRIOR FILING DATE: 1992-09-08

; PRIOR APPLICATION NUMBER: 07/624,515

; PRIOR FILING DATE: 1990-12-07

; PRIOR APPLICATION NUMBER: 07/189,814

; PRIOR FILING DATE: 1988-05-03

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 31

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence of the variable domain gene of

; OTHER INFORMATION: antibody D1.3 (Fig 7)

US-10-351-748-31

Query Match 76.2%; Score 550; DB 2; Length 135;

Best Local Similarity 77.2%; Pred. No. 1.5e-46;

Matches 105; Conservative 9; Mismatches 14; Indels 8; Gaps 1;

QY 1 MAVGLLLCLVTPSCVLSQVQLKESGPGLVAPQSLSITCTISGFSLTIDYGVHWVROP 60

Db 1 MAVLALLFCLVTPSCILSQVQLKESGPGLVAPQSLSITCTISGFSLTIDYGVHWVROP 60

QY 61 GKGLFWLVWSDGSSTVNSALKSRMTIRKDNKSQVFLINSLQTDSDAMVYCARHGTY 120

Db 61 GKGLFWLGMVWDGNDTNSALKSRSLISKDNKSQVFLKNSLHTDDTARYCARERDY 120

QY 121 YGMTTGTGALDYWGQ 136

Db 121 -----RLDYWGQ 128

RESULT 2

US-09-772-103-4

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	584	80.9	144	2	S11244	Ig gamma-2a chain
2	550.5	76.2	144	1	G2MS14	Ig heavy chain pre
3	539	74.7	141	2	S52446	Ig heavy chain v r
4	535.5	74.2	140	2	S55028	Ig heavy chain v r
5	533	73.8	135	2	S31913	Ig gamma-2A chain
6	523	72.4	117	2	S10111	Ig heavy chain v
7	520	72.0	139	2	A32456	Ig heavy chain pre
8	519	71.9	115	1	HVNS14	Ig heavy chain pre
9	499.5	69.2	140	2	S14238	Ig gamma-1 chain p
10	497	68.8	116	1	G1MS10	Ig heavy chain pre
11	496	68.7	116	2	A33932	Ig mu chain precu
12	477	66.1	101	2	S03466	Ig heavy chain v r
13	473	65.5	117	2	S38563	Ig heavy chain v r
14	473	65.5	122	2	S20809	Ig heavy chain v r
15	465	64.4	120	2	A43049	Ig heavy chain v r
16	460	63.7	120	2	PL0087	Ig heavy chain v r
17	458.5	63.5	112	2	S11100	Ig heavy chain v r
18	454.5	63.0	106	2	S14489	Ig heavy chain v r
19	454.5	63.0	114	2	S11106	Ig heavy chain v r
20	452.5	62.7	114	2	S11099	Ig heavy chain v r
21	448.5	62.1	116	2	S11102	Ig heavy chain v r
22	446.5	61.8	113	2	S11101	Ig heavy chain v r
23	445.5	61.7	111	2	S26324	Ig heavy chain v r
24	445.5	61.7	118	2	PQ2666	Ig gamma-2b chain
25	445.5	61.7	231	2	FC4155	Ig heavy chain v r
26	445	61.6	116	2	S42484	Ig heavy chain v r
27	444	61.5	107	2	S14492	Ig heavy chain v r
28	443.5	61.4	112	2	S11108	Ig heavy chain v r
29	443	61.4	118	2	S32786	Ig heavy chain (an

**A;Note: the authors tran**

Nature 286, 676-683, 1980  
A>Title: Two types of somatic recombination are necessary for the generation of complement C3c  
A:Reference number: A93229; PMID:81012133; PMID:6774258  
A:Accession: A02094  
A:Molecule type: DNA  
A:Residues: 1-144 <SAK>  
A:Cross-references: UNIPROT:P01819; UNIPARC:UPI000002726A; GB:V00768; GB:J00491; NID:91  
A>Note: The sequence shown was determined from a differentiated gene isolated from a myeloma cell line.  
A>Note: The authors translated the codon TAT for residue 51 as Thr and TTA for residue 52.  
C:Genetics:

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:25 ; Search time 62.9122 Seconds  
(without alignments)  
1999.647 Million cell updates/sec

Title: US-10-724-274-20

Perfect score: 722

Sequence: 1 MAVLGLLLCITFPFSCVLSQ.....HGTYGMMTTGDDALDYMCGQ 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	79.4	484	Q5u472_MOUSE	Q5u472 mus musculus
2	550.5	76.2	144	HV43_MOUSE	P01819 mus musculus
3	538	74.5	482	Q91X92_MOUSE	Q91X92 mus musculus
4	528	73.1	591	Q510L9_RAT	Q51019 rattus norv
5	519	71.9	115	HV44_MOUSE	P01820 mus musculus
6	517.5	71.7	469	Q5M839_RAT	Q5M839 rattus norv
7	509.5	70.6	477	Q510J1_RAT	Q510j1 rattus norv
8	501.5	69.5	458	Q5M842_RAT	Q5M842 rattus norv
9	497	68.8	116	HV45_MOUSE	P01821 mus musculus
10	451	62.5	121	Q99NG4_MOUSE	Q99ng4 mus musculus
11	376.5	52.1	135	HV02_XENLA	P20957 xenopus lae
12	373.5	51.7	560	Q4V801_XENLA	Q4v801 xenopus lae
13	370	51.2	485	Q561M5_MOUSE	Q561m5 mus musculus
14	369.5	51.2	483	Q5U413_MOUSE	Q5u413 mus musculus
15	367.5	50.9	487	Q58E53_MOUSE	Q58e53 mus musculus
16	364.5	50.5	485	Q58E54_MOUSE	Q58e54 mus musculus
17	360.5	49.9	476	Q6GMX1_HUMAN	Q6gmX1 homo sapien
18	359	49.7	617	Q569B3_RAT	Q569b3 rattus norv
19	357	49.4	615	Q569B6_RAT	Q569b6 rattus norv
20	355	49.2	477	Q6GMX7_HUMAN	Q6gmX7 homo sapien
21	353	48.9	465	Q6GMX6_HUMAN	Q6gmX6 homo sapien
22	351.5	48.7	136	HV01_XENLA	P20956 xenopus lae
23	350.5	48.5	136	Q6LBQ5_MOUSE	Q6lbQ5 mus musculus
24	348	48.2	496	Q96KX8_HUMAN	Q96kx8 homo sapien
25	345	47.8	482	Q5VLK6_RAT	Q5vlK6 rattus norv
26	344.5	47.7	573	Q8WU38_HUMAN	Q8wu38 homo sapien
27	344	47.6	620	Q96EY0_HUMAN	Q96ey0 homo sapien
28	343.5	47.6	493	Q569J1_HUMAN	Q569j1 homo sapien
29	342	47.4	137	HV46_MOUSE	P01822 mus musculus
30	341	47.2	576	Q6P4I8_HUMAN	Q6p4I8 homo sapien
31	340.5	47.2	595	Q3BBR4_RAT	Q3Bbr4 rattus norv

32 338 46.8 139 2 Q86SX2\_HUMAN Q86sx2 homo sapien  
33 337 46.7 478 2 Q7Z379\_HUMAN Q7z379 homo sapien  
34 335 46.4 467 2 Q4VBH1\_RAT Q4vbh1 rattus norv  
35 335 46.4 479 2 Q99M22\_MOUSE Q99m22 mus musculus  
36 333.5 46.2 121 1 HV3J\_HUMAN P01771 homo sapien  
37 332 46.0 116 1 HV61\_MOUSE P18532 mus musculus  
38 332 46.0 478 2 Q5FVQ3\_RAT Q5fvq3 rattus norv  
39 331 45.8 590 2 Q569B8\_RAT Q569b8 rattus norv  
40 330.5 45.8 119 2 Q9UL73\_HUMAN Q9ul73 homo sapien  
41 330 45.7 150 2 Q85973\_HUMAN Q85973 homo sapien  
42 329 45.6 118 2 Q811U5\_MOUSE Q811u5 mus musculus  
43 328 45.4 469 2 Q569F4\_HUMAN Q569f4 homo sapien  
44 327 45.3 116 1 HV60\_MOUSE P18531 mus musculus  
45 327 45.3 472 2 Q6N089\_HUMAN Q6n089 homo sapien

#### ALIGNMENTS

##### RESULT 1

Q5U472\_MOUSE PRELIMINARY; PRT; 484 AA.  
AC Q5U472;  
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE LOC544903 protein.  
GN Name=LOC544903;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Diatchenko L., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,  
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

##### NUCLEOTIDE SEQUENCE.

STRAIN=FVB/N; TISSUE=Colon;  
NIH MGC Project;  
Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.

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Distributed under the Creative Commons Attribution-NoDerivs License  
-----  
EMBL; BC085241; AAH85241.1; -; mRNA.  
DR Ensembl; ENSMUSG0000054328; Mus musculus.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG.cl.  
DR InterPro; IPR003006; IG.MHC.  
DR InterPro; IPR003596; IG\_v.



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 171.949 Seconds

(without alignments)  
1199.218 Million cell updates/sec

Title: US-10-724-274-25

Perfect score: 2400  
Sequence: 1 QVQLKSGPGLVAPQSLSI.....MHEALNNHYTKSLSLGK 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_8.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003s.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*
- 10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2400	100.0	451	8 ADQ31884	Adq31884 Antibody
2	2400	100.0	451	8 ADT77643	Adt77643 Antibody
3	2400	100.0	451	9 AEB51162	Aeb51162 Chimeric
4	2400	100.0	451	10 AEF12090	Aef12090 Anti-alpha
5	2397	99.9	451	8 ADT51711	Adt51711 M200 anti
6	2397	99.9	451	10 AEF16426	Aef16426 Chimeric
7	2394	99.8	451	8 ADT51709	Adt51709 M200 anti
8	2394	99.8	451	8 ADT51710	Adt51710 M200 anti
9	2394	99.8	451	10 AEF16425	Aef16425 Chimeric
10	2394	99.8	451	10 AEF16424	Aef16424 Chimeric
11	2391	99.6	451	8 ADT51712	Adt51712 M200 anti
12	2391	99.6	451	10 AEF16427	Aef16427 Chimeric
13	2389	99.5	451	8 ADT51713	Adt51713 M200 anti
14	2389	99.5	451	10 AEF16428	Aef16428 Chimeric
15	2282	95.1	451	8 ADQ31890	Adq31890 Antibody
16	2282	95.1	451	9 AEB51168	Aeb51168 Chimeric
17	2165.5	90.2	442	9 ADY74779	Ady74779 Rat anti-
18	2138.5	89.1	442	9 ADY74807	Ady74807 Rat anti-
19	2107.5	87.8	469	9 AEB45853	Aeb45853 Human mon
20	2107	87.8	462	9 AEB45881	Aeb45881 Human mon
21	2105.5	87.7	469	8 ADS16636	Adsl6636 Human ant
22	2100.5	87.5	465	9 AEB45849	Aeb45849 Human mon
23	2098.5	87.4	463	9 AEA41030	Aea41030 Human ant

Adf77154 Chimeric  
Adm41565 Anti-inte  
Aab49243 Chimeric  
Abr55342 Amino aci  
Adk52356 Human ant  
Aec20880 Low risk  
Aae27928 Human C5E  
Abb82837 Antibody  
Adl93669 Human CD4  
Adm41559 Anti-inte  
Adl93662 Human CD4  
Aaw13564 Humanised  
Adl93663 Human CD4  
Aec40039 Heavy cha  
Adl93670 Human CD4  
Aea41064 Human ant  
Aea41047 Human ant  
Aea41062 Human ant  
Adl93667 Human CD4  
Adg93783 Monoclonal  
Adul7617 Human ant  
Adul7474 Human ant

#### ALIGNMENTS

##### RESULT 1

ADQ31884  
ID ADQ31884 standard; protein; 451 AA.

XX ADQ31884;

XX 23-SEP-2004 (first entry)

DE Antibody M200 heavy chain amino acid sequence SEQ ID NO:25.

XX chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;  
KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;  
KW vascularisation; antiangiogenic; integrin alpha5beta1 antagonist.

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

XX WO2004056308-A2.

XX 08-JUL-2004.

XX 26-NOV-2003; 2003WO-US038172.

XX 26-NOV-2002; 2002US-0429743P.

XX (PROT-) PROTEIN DESIGN LABS INC.

PI Ramakrishnan V, Powers D, Johnson DE, Jeffrey U;

DR WPI; 2004-525316/50.

XX N-PSDB; ADQ31882.

PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling  
vascularization in injured tissue.

PS Claim 23; SEQ ID NO 25; 89pp; English.

XX The present invention describes a chimeric anti-alpha5beta-1 integrin  
antibody (I), comprising: (a) a first polypeptide sequence from SEQ ID  
source comprising one or more amino acid sequences selected from SEQ ID  
NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second  
polypeptide from a second source comprising a constant region sequence of  
an antibody of the second source, where the first and second polypeptide  
sequences form a protein complex that is immunoreactive with alpha5beta1  
integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 26.9954 Seconds  
(without alignments)  
1607.447 Million cell updates/sec

Title: US-10-724-274-25  
Perfect score: 2400  
Sequence: 1 QVQLKESGGLVAPSSQSLSI.....MHEALHNHYTQKSLSLGLK 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1743	72.6	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	66.9	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.3	330	1 GHU	Ig gamma-1 chain C
4	1585	66.0	377	2 A60764	Ig gamma-3 chain C
5	1575	65.6	377	2 A23511	Ig gamma-3 chain C
6	1554	64.8	470	2 S22080	Ig heavy chain pre
7	1519	63.3	472	2 P31459	Ig gamma-1 chain -
8	1423.5	59.3	444	2 P4436	monoclonal antibody
9	1417	59.0	446	2 S40295	Ig gamma-2a chain
10	1412.5	58.9	469	2 S37483	Ig gamma-2a chain
11	1411	58.8	374	2 S89339	Ig heavy chain v r
12	1305	54.4	474	1 G2MS11	Ig gamma-2b chain
13	1289.5	53.7	328	2 I47159	Ig gamma 2a chain
14	1289.5	53.7	475	2 S01321	Ig gamma-2b chain
15	1283.5	53.5	328	2 I47160	Ig gamma 2b chain
16	1264.5	52.7	328	2 I47161	Ig gamma 1 chain c
17	1240.5	51.7	328	2 I47158	Ig gamma 1 chain c
18	1199	50.0	323	1 GHRB	Ig gamma chain C r
19	1162	48.4	329	1 G3GP	Ig gamma-2 chain C
20	1147	47.8	308	2 C30554	Ig heavy chain C r
21	1139.5	47.5	255	4 S31866	Ig gamma-1 chain C
22	1139.5	47.1	234	2 PT0207	Ig gamma chain C r
23	1124	46.8	333	2 P80018	Ig gamma-2b chain C
24	1118.5	46.6	326	2 P80017	Ig gamma-1 chain C
25	1108.5	46.2	289	1 G3HUW1	Ig gamma-3 heavy c
26	1108	46.2	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.1	324	1 G1MS	Ig gamma-1 chain C
28	1106.5	46.1	330	1 G2MSA	Ig gamma-2a chain
29	1103	46.0	327	2 S06611	Ig gamma-2 chain C

30	1101.5	45.9	393	1 G1MSM	Ig gamma-1 chain C
31	1101.5	45.9	399	1 G2MSAM	Ig gamma-2a chain
32	1099	45.8	335	1 G2MSAB	Ig gamma-2a chain
33	1098.5	45.8	329	1 G3MSC	Ig gamma-3 chain C
34	1090.5	45.4	398	1 G3MSM	Ig gamma-3 chain C
35	1085.5	45.2	277	2 I47162	Ig gamma 4 chain c
36	1084.5	45.2	322	2 P80019	Ig gamma-2a chain
37	1049.5	43.7	405	1 G2MSBM	Ig gamma-2b chain
38	942	39.2	548	2 S38864	Ig epsilon chain C
39	845.5	35.2	549	2 S04845	Ig heavy chain pre
40	797	33.2	231	2 PC4155	Ig gamma-2b chain
41	790.5	32.9	241	2 S69131	Ig heavy chain (DO
42	785.5	32.7	220	2 A49444	Ig gamma-1 heavy c
43	769.5	32.1	572	2 B46529	Ig y heavy chain (
44	760	31.7	592	2 S25705	Ig mu chain - shee
45	749.5	31.2	249	2 S69340	Ig heavy chain VHI

ALIGNMENTS

RESULT 1

G4HU  
IG gamma-4 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004  
C;Accession: A90333; A90249; A02150  
R;Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A;Reference number: A90933; MUID:83157104; PMID:6299662  
A;Accession: A90933  
A;Molecule type: DNA  
A;Residues: 1-327 <ELL>  
A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190  
A;Note: the sequence was determined from the Germline gene  
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A;Reference number: A90249; MUID:70207560; PMID:4192699  
A;Accession: A90249  
A;Molecule type: protein  
A;Residues: 1-30;81-326 <PIN>  
A;Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796  
C;Genetics:  
A;Gene: GDB:IGHG4  
A;Cross-references: GDB:119340; OMIM:147130  
A;Map position: 14q32.33-14q32.33  
A;Introns: 99/1; 111/1; 221/1  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into : C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMI>  
F;99-110/Region: hinge  
F;134-203/Domain: immunoglobulin homology <IM2>  
F;240-307/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83,141-201,247-305/Disulfide bonds: #status predicted  
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;177/Binding site: carbohydrate (Asn) #status predicted

Query Match 72.6%; Score 1743; DB 1; Length 327;  
Best Local Similarity 100.0%; Pred. No. 5.5e-95;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	125	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	184
Db	1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS	60
Qy	185	GLYSLSSVTVTPSSSLGKTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPSV	244
Db	61	GLYSLSSVTVTPSSSLGKTQYTCNVDPKPSNTKVDKRVESKYGPPCPSCPAPEFLGSPSV	120

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 6, 2006, 04:37:25 ; Search time 208.628 Seconds  
(without alignments)  
1999.647 Million cell updates/sec  
Title: US-10-724-274-25  
Perfect score: 2400  
Sequence: 1 QVQLKESGFLVAPSSQSLSI.....MHEALHNHYTQKSLSLGLK 451

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Uniprot 7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041.5	85.1	475	2 Q6MXZ7_HUMAN	Q6mxz7 homo sapien
2	2014	83.9	473	2 Q8TC63_HUMAN	Q8tc63 homo sapien
3	1948	81.2	476	2 Q6GMX1_HUMAN	Q6gmX1 homo sapien
4	1943	81.0	472	2 Q6N089_HUMAN	Q6n089 homo sapien
5	1939.5	80.8	465	2 Q6GMX6_HUMAN	Q6gmX6 homo sapien
6	1939.5	80.8	469	2 Q569F4_HUMAN	Q569f4 homo sapien
7	1918	79.9	478	2 Q6P181_HUMAN	Q6p181 homo sapien
8	1916	79.8	470	2 Q6PJ44_HUMAN	Q6pj44 homo sapien
9	1914.5	79.8	465	2 Q6P6C4_HUMAN	Q6p6c4 homo sapien
10	1912	79.7	464	2 Q6MZU6_HUMAN	Q6mzu6 homo sapien
11	1905	79.4	466	2 Q6IN78_HUMAN	Q6in78 homo sapien
12	1902	79.2	470	2 Q7Z5W1_HUMAN	Q7z5w1 homo sapien
13	1900.5	79.2	475	2 Q5EF85_HUMAN	Q5efe5 homo sapien
14	1896.5	79.0	544	2 Q6PJ95_HUMAN	Q6pj95 homo sapien
15	1894	78.9	470	2 Q6PCN4_HUMAN	Q6pcn4 homo sapien
16	1891.5	78.8	473	2 Q6MZV7_HUMAN	Q6mzv7 homo sapien
17	1891	78.8	482	2 Q7Z351_HUMAN	Q7z351 homo sapien
18	1886	78.6	480	2 Q6N094_HUMAN	Q6n094 homo sapien
19	1882.5	78.4	475	2 Q6GMW7_HUMAN	Q6gmw7 homo sapien
20	1877.5	78.2	481	2 Q6N097_HUMAN	Q6n097 homo sapien
21	1877	78.2	466	2 Q6N096_HUMAN	Q6n096 homo sapien
22	1870.5	77.9	475	2 Q6MZQ6_HUMAN	Q6mzq6 homo sapien
23	1869.5	77.9	475	2 Q6N095_HUMAN	Q6n095 homo sapien
24	1866.5	77.8	473	2 Q6P055_HUMAN	Q6p055 homo sapien
25	1856.5	77.4	521	2 Q8N4Y9_HUMAN	Q8n4y9 homo sapien
26	1851.5	77.1	519	2 Q5EBM2_HUMAN	Q5ebm2 homo sapien
27	1848	77.0	417	2 Q6N093_HUMAN	Q6n093 homo sapien
28	1838	76.6	518	2 Q6N030_HUMAN	Q6n030 homo sapien
29	1829	76.2	480	2 Q6PJF1_HUMAN	Q6pjf1 homo sapien
30	1821.5	75.9	469	2 Q7Z7P5_HUMAN	Q7z7p5 homo sapien
31	1820.5	75.9	475	2 Q5RE17_PONPY	Q5re17 pongo pygma

RESULT 1  
ID Q6MXZ7\_HUMAN PRELIMINARY; PRT; 476 AA.  
AC Q6MXZ7; 2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DB Hypothetical protein DKFZp686M24218.  
GN Name=DKFZp686M24218;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Tissue=Human rectum tumor;  
RG The German Human cDNA Consortium;  
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Oeanger A.,  
RA Pobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

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EMBL; BX640824; CAB45900.1; -; mRNA.  
HSSP; P01861; 1ADQ.  
SMR; Q6MXZ7; 28-472.  
InterPro; IPR003599; IG-like.  
InterPro; IPR007110; IG-like.  
InterPro; IPR003597; IG-cl.  
InterPro; IPR003006; IG\_MHC.  
InterPro; IPR003596; IG\_v.  
InterPro; IPR013106; V-set.  
Pfam; PF07654; Cl-set; 3.  
SMART; SM00409; IG; 1.  
SMART; SM00407; IGC1; 2.  
SMART; SM00406; IGV; 1.  
PROSITE; PS50835; IG LIKE; 4.  
PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1PFES85958F CRC64;

Query Match 85.1%; Score 2041.5; DB 2; Length 476;  
Best Local Similarity 85.0%; Pred. No. 4.1e-135;  
Matches 385; Conservative 25; Mismatches 38; Indels 5; Gaps 2;  
QY 1 QVQLKESGFLVAPSSQSLSICTISGFLSLTDYGVH--WVRQPPGKGLVIVLWVDSGSET 58  
27 QLQLQESGFLVKSAFTLSLTCVDPGYLSDSSSSYGMWIRQPPGGLGIVTYSVSGTYP 86  
Db 59 YNSALKSRMTIRKONSKSQVFLINLSQTDSDSAMTYCARHGTYGWTGTTGDALDVGQGT 118  
QY 87 YTPSLKSLRTIHVDPSPKSKQIFLNLTSVTAADTAVTYCVRHG---GYSFASAYFPFWGQGA 143  
Db



GehCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 88.4528 Seconds  
(without alignments)  
1199.218 Million cell updates/sec

Title: US-10-724-274-28  
Perfect score: 1225  
Sequence: 1 QVQKESGPGLVAPQSLSI.....PSNTKVDKRVESKYGPPCPSS 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 18.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*  
10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	100.0	232	8 ADQ31887	Adg31887 Antibody
2	1225	100.0	232	8 ADT77646	Adt77646 Antibody
3	1225	100.0	232	8 AEB51165	Aeb51165 Chimeric
4	1225	100.0	451	8 ADQ31884	Adg31884 Antibody
5	1225	100.0	451	8 ADT51712	Adt51712 M200 anti
6	1225	100.0	451	8 ADT51711	Adt51711 M200 anti
7	1225	100.0	451	8 ADT51709	Adt51709 M200 anti
8	1225	100.0	451	8 ADT51713	Adt51713 M200 anti
9	1225	100.0	451	8 ADT51710	Adt51710 M200 anti
10	1225	100.0	451	8 ADT77643	Adt77643 Antibody
11	1225	100.0	451	9 AEB51162	Aeb51162 Chimeric
12	1225	100.0	451	9 AEF12090	Aef12090 Anti-alph
13	1225	100.0	451	10 AEF16428	Aef16428 Chimeric
14	1225	100.0	451	10 AEF16425	Aef16425 Chimeric
15	1225	100.0	451	10 AEF16426	Aef16426 Chimeric
16	1225	100.0	451	10 AEF16427	Aef16427 Chimeric
17	1225	100.0	451	10 AEF16424	Aef16424 Chimeric
18	1107	90.4	451	8 ADQ31890	Adg31890 Antibody
19	1107	90.4	451	9 AEB51168	Aeb51168 Chimeric
20	997	81.4	462	8 ADT77154	Adt77154 Rat anti-
21	990.5	80.9	442	9 ADT74779	Adt74779 Rat anti-
22	981.5	80.1	476	4 AAB49243	Aab49243 Chimeric
23	978.5	79.9	468	5 AAE27928	Aae27928 Human CSE

## ALIGNMENTS

### RESULT 1

ADQ31887  
ID ADQ31887 standard; protein; 232 AA.

XX ADQ31887;

XX 23-SEP-2004 (first entry)

XX Antibody F200 heavy chain amino acid sequence SEQ ID NO:28.

XX chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;  
KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;  
KW vascularisation; antiangiogenic; integrin alpha5beta5 antagonist.

OS Mus sp.  
OS Homo sapiens.  
OS Synthetic.

XX WO2004056308-A2.

XX PD 08-JUL-2004.

XX PF 26-NOV-2003; 2003WO-US038172.

XX 26-NOV-2002; 2002US-0429743P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Ramakrishnan V, Powers D, Johnson DB, Jeffrey U;

XX WPI; 2004-525316/50.

XX N-PSDB; ADQ31886.

XX New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling

XX vascularisation in injured tissue.

XX Claim 23; SEQ ID NO 28; 89pp; English.

XX The present invention describes a chimeric anti-alpha5beta-1 integrin  
XX antibody (I), comprising: (a) a first polypeptide sequence from a first  
XX source comprising one or more amino acid sequences selected from SEQ ID  
XX NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second  
XX polypeptide from a second source comprising a constant region sequence of  
XX an antibody of the second source, where the first and second polypeptide  
XX sequences form a protein complex that is immunoreactive with alpha5beta1  
XX integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

Abb82837 Antibody  
Aae27929 Human CH2  
Abb82838 Antibody  
Ady74807 Rat anti-  
Aar21261 VHD1.3-Hu  
Adul7617 Human ant  
Adul7474 Human ant  
Aea48171 Mouse ant  
Aea48171 Mouse ant  
Aad14299 EGFR anti  
Adp44637 Murine an  
Aea60463 Mouse ant  
Aeb45853 Human mon  
Aeb45881 Human mon  
Aq17121 Humanised  
Aea41030 Human ant  
Aeb45849 Human mon  
Aad16636 Human ant  
Aad15655 Anti-inte  
Aef22802 Cetuximab  
Aab81972 Gangliosid  
Adq98104 Chimeric

24 978.5 79.9 468 6 ABB82837  
25 977.5 79.8 358 5 AAE27929  
26 977.5 79.8 358 6 ABB82838  
27 963.5 78.7 442 9 ADY74807  
28 963 78.6 241 2 AAR21261  
29 961 78.4 469 8 ADU17617  
30 961 78.4 469 8 ADU17474  
31 956 78.0 446 9 AEA48171  
32 943.5 77.0 488 8 ADS14299  
33 935.5 76.4 782 8 ADP44637  
35 935.5 76.4 782 9 AEA60463  
36 932.5 76.1 469 9 AEB45853  
37 932 76.1 462 9 AEB45881  
38 931 76.0 447 8 ADQ17121  
39 930.5 76.0 463 9 AEA41030  
40 930.5 76.0 465 9 AEB45849  
41 930.5 76.0 469 8 ADS16636  
42 929 75.8 466 8 ADM41565  
43 925.5 75.6 220 10 AEF22802  
44 925 75.5 581 4 AAB81972  
45 922 75.3 254 8 ADQ98104

Sequence 4, Appli  
Sequence 222, App  
Sequence 224, App  
Sequence 224, App  
Sequence 224, App  
Sequence 210, App  
Sequence 220, App  
Sequence 238, App  
Sequence 240, App  
Sequence 242, App  
Sequence 244, App  
Sequence 246, App  
Sequence 210, App  
Sequence 220, App  
Sequence 238, App  
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Sequence 242, App  
Sequence 244, App  
Sequence 246, App  
Sequence 210, App  
Sequence 220, App  
Sequence 238, App  
Sequence 240, App  
Sequence 242, App  
Sequence 244, App  
Sequence 246, App

27 840 68.6 473 2 US-09-049-672A-4  
28 838 68.4 450 2 US-09-996-288-222  
29 838 68.4 450 2 US-09-996-288-224  
30 838 68.4 450 2 US-09-996-265-222  
31 838 68.4 450 2 US-09-996-265-224  
32 836 68.2 450 2 US-09-996-288-210  
33 836 68.2 450 2 US-09-996-288-220  
34 836 68.2 450 2 US-09-996-288-238  
35 836 68.2 450 2 US-09-996-288-240  
36 836 68.2 450 2 US-09-996-288-242  
37 836 68.2 450 2 US-09-996-288-244  
38 836 68.2 450 2 US-09-996-265-210  
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40 836 68.2 450 2 US-09-996-265-238  
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43 836 68.2 450 2 US-09-996-265-244  
44 836 68.2 450 2 US-09-996-265-246  
45 836 68.2 450 2 US-09-996-265-246

ALIGNMENTS

RESULT 1  
US-09-726-219A-187  
; Sequence 187, Application US/09726219A  
; Patent No. 6806079  
; GENERAL INFORMATION:  
; APPLICANT: Cambridge Antibody Technology Limited  
; APPLICANT: Medical Research Council  
; APPLICANT: McCafferty, John  
; APPLICANT: Pope, Anthony  
; APPLICANT: Johnson, Kevin  
; APPLICANT: Hoogenboom, Hendricus  
; APPLICANT: Griffiths, Andrew  
; APPLICANT: Jackson, Ronald  
; APPLICANT: Holliger, Kasper  
; APPLICANT: Marks, James  
; APPLICANT: Clackson, Timothy  
; APPLICANT: Chiswell, David  
; APPLICANT: Winter, Gregory  
; APPLICANT: Bonert, Timothy  
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs  
; FILE REFERENCE: 213839-00013  
; CURRENT APPLICATION NUMBER: US/09/726,219A  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: GB 9015198.6  
; PRIOR FILING DATE: 1990-07-10  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9022845.3  
; PRIOR FILING DATE: 1990-10-19  
; PRIOR APPLICATION NUMBER: GB 9024503.6  
; PRIOR FILING DATE: 1990-11-12  
; PRIOR APPLICATION NUMBER: GB 9104744.9  
; PRIOR FILING DATE: 1991-03-06  
; PRIOR APPLICATION NUMBER: GB 9110549.4  
; PRIOR FILING DATE: 1991-05-15  
; PRIOR APPLICATION NUMBER: PCT/GB91/01134  
; PRIOR FILING DATE: 1991-07-10  
; PRIOR APPLICATION NUMBER: US 07/971,857  
; PRIOR FILING DATE: 1993-01-08  
; PRIOR APPLICATION NUMBER: US 08/484,893  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 272  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 187  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

Sequence 187, App  
Sequence 187, App  
Sequence 7, Appli  
Sequence 6, Appli  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 66, Appli  
Sequence 81, Appli  
Sequence 4, Appli  
Sequence 68, Appli  
Sequence 5, Appli  
Sequence 1, Appli  
Sequence 63, Appli  
Sequence 110, App  
Sequence 8, Appli  
Sequence 10, Appli  
Sequence 12, Appli  
Sequence 45, Appli  
Sequence 68, Appli  
Sequence 41, Appli  
Sequence 42, Appli  
Sequence 32, Appli  
Sequence 36, Appli

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 6, 2006, 04:59:30 ; Search time 24.4528 Seconds  
(without alignments)  
830.460 Million cell updates/sec  
Title: US-10-724-274-28  
Perfect score: 1225  
Sequence: 1 QVQLKESGFLVAPSOISL.....PSNTKVDKRVESKIGPPCPS 232  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Issued Patents AA:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	963.	78.6	241	2	US-09-726-219A-187
2	963	78.6	241	2	US-09-196-522-187
3	917	74.9	446	2	US-08-397-411-7
4	909	74.2	273	2	US-08-397-411-6
5	897	73.2	443	5	PCT-US96-13152-4
6	889	72.6	464	2	US-09-472-087-2
7	889	72.6	464	2	US-09-472-087-66
8	888.5	72.5	467	1	US-08-704-744-81
9	885	72.2	451	2	US-09-472-087-70
10	884.5	72.2	463	2	US-09-472-087-4
11	884.5	72.2	460	2	US-10-630-406-5
12	883	72.1	463	2	US-09-472-087-1
13	878.5	71.7	463	2	US-09-472-087-63
14	878.5	71.7	463	2	US-09-472-087-64
15	878.5	71.7	463	2	US-10-194-975-110
16	876	71.5	250	2	US-08-523-894-8
17	858.5	70.1	467	2	US-08-523-894-10
18	855.5	69.8	467	2	US-08-523-894-12
19	854.5	69.6	467	1	US-07-916-098A-45
20	853	69.6	225	2	US-09-456-090A-68
21	852.5	69.6	225	2	US-09-453-234-68
22	852.5	69.6	225	2	US-08-030-175-41
23	848	69.2	467	2	US-08-030-175-41
24	844	68.9	467	2	US-08-030-175-42
25	840	68.6	470	2	US-09-859-053-32
26	840	68.6	470	2	US-09-859-053-36

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 13.868 Seconds  
(without alignments)

1607.447 Million cell updates/sec

Title: US-10-724-274-28

Perfect score: 1225

Sequence: 1 QVQLKESGPGLVAPSSQSLST.....PSNTKVDKRVESKYGPPCPFS 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\* ;

1: Pirl.\* ;

2: Pirl.\* ;

3: Pirl.\* ;

4: Pirl.\* ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	789	64.4	231	2	PC4155
2	785.5	64.1	220	2	A49444
3	750.5	61.3	241	2	S69131
4	721	58.9	470	2	S22080
5	694	56.7	472	2	S31459
6	660	53.9	246	2	S38950
7	660	53.9	446	2	S40295
8	640.5	52.3	469	2	S37483
9	631.5	51.6	444	2	PC4436
10	626.5	51.1	220	2	S68211
11	620.5	50.7	548	2	S38864
12	611	49.9	213	2	S88213
13	578.5	47.2	475	2	S01321
14	577	47.1	221	2	S49220
15	575.5	47.0	214	2	PC4202
16	573.5	46.8	254	2	B31790
17	568	46.4	327	1	G4HU
18	567	46.3	474	1	G2MS11
19	552	45.1	549	2	S04845
20	529	43.2	144	2	S11244
21	513.5	41.9	326	1	G2HU
22	508.5	41.5	140	2	S14238
23	503	41.1	122	2	S20809
24	501	40.9	377	2	A23511
25	501	40.9	377	2	A60764
26	500.5	40.9	144	1	G2MS14
27	499	40.7	117	2	S38563
28	498	40.7	122	2	A49049
29	496	40.5	592	2	S25705

#### RESULT 1

PC4155

Ig gamma-2b chain V-C region MabB23 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 21-Jan-2000

C;Accession: PC4155

R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.

Gene 169, 237-239, 1996

A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a n

A;Reference number: PC4155; MUID:96194809; PMID:8647454

A;Accession: PC4155

A;Molecule type: mRNA

A;Residues: 1-231 <KWA>

A;Cross-references: UNIPARC:UPI00001157CB; GB:U28970; NID:G1262180; PIDN:AAC52489.1; P;

A;Note: This protein has unusual amino acid compared with the conserved sequences of m

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;1-231/Product: heavy chain #status predicted <MAT>

F;98-102/Region: unique D sequence

F;103-119/Region: V region

F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 64.4%; Score 789; DB 2; Length 231;  
Best Local Similarity 66.5%; Pred. No. 1.9e-47;  
Matches 157; Conservative 26; Mismatches 41; Indels 12; Gaps 4;

Qy 1 QVQLKESGPGLVAPSSQSLSTCTISGFSITDYGVHVRQPPGKGLVWLVWSDGSSSTYN 60

Db 1 EVQLVESGPGLVAPSSQSLSTCTVSGFSLTDYGVSWIRQPPGKGLVWLVWAGSSTFTYN 60

Qy 61 SALKSRVTIRKDNKSQVFLIMNSLOTDDSAMVYCARHGTYYGTTTTGDALDYWGQTSV 120

Db 61 SALKSRUSIKDNKSQVFLKNSLHDDTDYNYCVKHEDRYDW-----YFDVWGAGITV 115

Qy 121 TVSSASTKGPSVFPPLPCSRSTSESTAALGLVVDYPPPEPTVSNVNSGALSGVHTTPAV 180

Db 116 TVSSAKTPPSVYPLAPRCGDTTGSVTLGLVKGYPPESTVTWNSGSLSSSVHTPPAL 175

Qy 181 LQSSGLVSLSSVTVPPSSSLGKTYYTCNVDPKPNKVDKRVESKYGP-----PCP 231

Db 176 LQ-SGLYTMSSSVTVPPSTWPSQTVCVAHPASSTTVDDKKLSPS-GPSTINPCP 229

#### RESULT 2

A49444

Ig gamma-1 heavy chain (New) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999

C;Accession: A49444

R;Saul, F.A.; Poljak, R.J.

Proteins 14, 363-371, 1992

A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A r

A;Reference number: A49444; MUID:93066153; PMID:1438175

Result No.	Score	Query Match	Length	DB	ID	Description	
1	875.5	71.5	476	2	Q6MZX7	HUMAN sapien	
2	844.5	68.9	476	2	Q6GNX1	HUMAN sapien	
3	839.5	68.5	472	2	Q6N089	HUMAN sapien	
4	839	68.5	473	2	Q8TC63	HUMAN sapien	
5	836	68.2	465	2	Q6GNX6	HUMAN sapien	
6	836	68.2	469	2	Q569F4	HUMAN sapien	
7	827.5	67.6	464	2	Q6PEC4	HUMAN sapien	
8	823	67.2	464	2	Q6MZU6	HUMAN sapien	
9	816	66.6	470	2	Q6CN44	HUMAN sapien	
10	812.5	66.3	470	2	Q6PUA4	HUMAN sapien	
11	808.5	66.0	478	2	Q6P181	HUMAN sapien	
12	801.5	65.4	466	2	Q6IN78	HUMAN sapien	
13	801	65.4	544	2	Q6PU95	HUMAN sapien	
14	798.5	65.2	470	2	Q725W1	HUMAN sapien	
15	797	65.1	475	2	Q5EPES	HUMAN sapien	
16	791.5	64.6	482	2	Q73351	HUMAN sapien	
17	788	64.3	469	2	Q5MB39	RATUS norv	
18	786.5	64.2	480	2	Q6N094	HUMAN sapien	
19	782	63.8	472	2	Q6MZV7	HUMAN sapien	
20	780.5	63.7	466	2	Q6N096	HUMAN sapien	
21	779.5	63.6	521	2	Q8N4Y9	HUMAN sapien	
22	779	63.6	475	2	Q6GNW7	HUMAN sapien	
23	778	63.5	481	2	Q6N097	HUMAN sapien	
24	777.5	63.5	519	2	Q5EBM2	HUMAN sapien	
25	777	63.4	475	2	Q6N095	HUMAN sapien	
26	772	63.0	458	2	Q5M842	RATUS norv	
27	771	62.9	475	2	Q6MQ66	HUMAN sapien	
28	767	62.6	473	2	Q6P055	HUMAN sapien	
29	764	62.4	518	2	Q6N030	HUMAN sapien	
30	756	61.7	477	2	Q6N093	HUMAN sapien	
31	733	59.8	475	2	Q5RE17	PONPY pongo pygma	

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:37:11 ; Search time 171.949 Seconds  
(without alignments)  
1199.218 Million cell updates/sec

Title: US-10-724-274-31

Perfect score: 2399

Sequence: 1 EVLVESGGGLVQPGSLRL.....MHEALHHYTKLSLSLGLK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: Geneseqp2002s:  
6: Geneseqp2003as:  
7: Geneseqp2003bs:  
8: Geneseqp2004s:  
9: Geneseqp2005s:  
10: Geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2399	100.0	451	ADQ31890	Adq31890 Antibody
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3	2282	95.1	451	ADQ31884	Adq31884 Antibody
4	2282	95.1	451	ADT77643	Adt77643 Antibody
5	2282	95.1	451	AE511162	Ae511162 Chimeric
6	2282	95.1	451	AEF12090	Aef12090 Anti-alpha
7	2279	95.0	451	ADT51711	Adt51711 M200 anti
8	2279	95.0	451	AEF16426	Aef16426 Chimeric
9	2276	94.9	451	ADT51709	Adt51709 M200 anti
10	2276	94.9	451	ADT51710	Adt51710 M200 anti
11	2276	94.9	451	AEF16425	Aef16425 Chimeric
12	2276	94.9	451	AEF16424	Aef16424 Chimeric
13	2273	94.7	451	ADT51712	Adt51712 M200 anti
14	2273	94.7	451	AEF16427	Aef16427 Chimeric
15	2271	94.7	451	ADT51713	Adt51713 M200 anti
16	2271	94.7	451	AEF16428	Aef16428 Chimeric
17	2206.5	92.0	444	ABR55342	Ab55342 Amino aci
18	2209.5	91.7	462	AE545881	Ae545881 Human mon
19	2199.5	91.7	469	ADSL16636	Adsl16636 Human ant
20	2192.5	91.4	463	AEA41030	Aea41030 Human ant
21	2189	91.2	443	AAW13564	Aaw13564 Humanised
22	2188.5	91.2	469	AE545853	Ae545853 Human mon
23	2187.5	91.2	469	ADL93669	Adl93669 Human CD4

24	2186.5	91.1	465	9	AE445849	Aeb45849 Human mon
25	2183	91.0	466	8	ADM41565	Adm41565 Anti-inte
26	2182.5	91.0	469	8	ADL93662	Human CD4
27	2177	90.7	464	8	ADL93663	Human CD4
28	2175	90.7	447	9	AEC40039	Heavy cha
29	2172.5	90.6	465	7	ADD93783	Ad93783 Monoclonal
30	2171	90.5	466	8	ADM41559	Anti-inte
31	2170	90.5	462	8	ADL93670	Human CD4
32	2170	90.5	466	8	ADL93667	Human CD4
33	2169.5	90.4	461	9	AEA41064	Human ant
34	2169.5	90.4	461	9	AEA41047	Human ant
35	2168	90.4	460	8	ADL93664	Human CD4
36	2166.5	90.3	467	2	AAR80617	Plasemid p
37	2166	90.3	460	8	ADJ55026	Adj55026 Anti-huma
38	2165	90.2	462	8	ADL93660	Human CD4
39	2164.5	90.2	461	9	AEA41056	Human ant
40	2164.5	90.2	461	9	AEA41055	Human ant
41	2164	90.2	468	8	ADL93666	Human CD4
42	2161	90.1	462	8	ADL93668	Human CD4
43	2160.5	90.1	461	9	AEA41062	Human ant
44	2160	90.0	464	8	ADL93661	Human ant
45	2159.5	90.0	467	9	AEA41068	Human ant

## ALIGNMENTS

### RESULT 1

ADQ31890  
ID ADQ31890 standard; protein; 451 AA.

AC ADQ31890;

DT 23-SEP-2004 (first entry)

DE Antibody hum200 heavy chain amino acid sequence SEQ ID NO:31.

XX chimeric anti-alpha5beta-1 integrin antibody; antibody; immunoreactive;  
KW alpha5beta1 integrin; humanised anti-alpha5beta1 integrin antibody;  
KW vascularisation; antiangiogenic; integrin alpha5beta1 antagonist.

OS Mus sp.

OS Homo sapiens.

OS Synthetic.

PN WO2004056308-A2.

XX 08-JUL-2004.

XX 26-NOV-2003; 2003WO-US038172.

XX 26-NOV-2002; 2002US-0429743P.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Ramakrishnan V, Powers D, Johnson DE, Jeffrey U;

DR WPI; 2004-525316/50.

DR N-PSDB; ADQ31888.

PT New chimeric anti-alpha-5 beta-1 integrin antibody useful for controlling  
PT vascularization in injured tissue.

XX Claim 23; SEQ ID NO 31; 89pp; English.

XX The present invention describes a chimeric anti-alpha5beta-1 integrin  
CC antibody (I), comprising: (a) a first polypeptide sequence from a first  
CC source comprising one or more amino acid sequences selected from SEQ ID  
CC NOS: 1, 7, 16, 18, 20, 22, 25, 26, 28, 31 and 32; and (b) a second  
CC polypeptide from a second source comprising a constant region sequence of  
CC an antibody of the second source, where the first and second polypeptide  
CC sequences form a protein complex that is immunoreactive with alpha5beta1  
CC integrin. Also described: (1) purifying (M1) pH-sensitive (I) comprises

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OM protein - protein search, using sw model

Run on: June 6, 2006, 04:59:30 ; Search time 47.5355 Seconds  
(without alignments)  
830.460 Million cell updates/sec

Title: US-10-724-274-31

Perfect score: 2399

Sequence: 1 EVOLVESGGGLVQPGGSLRL.....MPEALHHVTKQSLSLGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

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- 3: /EMC\_Celerra\_SID3S/ptodata/2/iaa/7\_COMB.pep.\*
- 4: /EMC\_Celerra\_SID3S/ptodata/2/iaa/H\_COMB.pep.\*
- 5: /EMC\_Celerra\_SID3S/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /EMC\_Celerra\_SID3S/ptodata/2/iaa/RE\_COMB.pep.\*
- 7: /EMC\_Celerra\_SID3S/ptodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2189	91.2	443	5	PCT-US96-13152-4
2	2166.5	90.3	467	1	US-08-704-744-81
3	2166	90.3	460	2	US-10-630-406-5
4	2067.5	86.2	467	1	US-07-916-098A-45
5	2066	86.1	464	2	US-09-472-087-2
6	2066	86.1	464	2	US-09-472-087-66
7	2063	86.0	451	2	US-09-472-087-70
8	2058.5	85.8	463	2	US-09-472-087-4
9	2058.5	85.8	463	2	US-09-472-087-68
10	2053.5	85.6	463	2	US-09-472-087-1
11	2053.5	85.6	463	2	US-09-472-087-63
12	2047.5	85.3	463	2	US-09-472-087-64
13	2034.5	84.8	467	2	US-08-523-894-8
14	2033	84.7	451	2	US-09-925-179-66
15	2032	84.7	470	2	US-09-859-053-32
16	2032	84.7	470	2	US-09-859-053-36
17	2032	84.7	474	2	US-09-848-832-3
18	2031.5	84.7	444	2	US-10-147-849-7
19	2030	84.6	451	1	US-08-887-352B-14
20	2030	84.6	451	1	US-08-887-352B-16
21	2030	84.6	451	2	US-08-466-151-65
22	2030	84.6	451	2	US-09-109-207C-14
23	2030	84.6	451	2	US-09-109-207C-16
24	2030	84.6	451	2	US-09-296-005-14
25	2030	84.6	451	2	US-09-296-005-16
26	2030	84.6	451	2	US-09-920-171-14

27	2030	84.6	451	2	US-09-920-171-16	Sequence 16, Appl
28	2030	84.6	451	2	US-09-716-028-14	Sequence 14, Appl
29	2030	84.6	451	2	US-09-716-028-16	Sequence 16, Appl
30	2030	84.6	451	2	US-10-113-996-14	Sequence 14, Appl
31	2030	84.6	451	2	US-10-113-996-16	Sequence 16, Appl
32	2030	84.6	451	2	US-09-925-179-65	Sequence 65, Appl
33	2029.5	84.6	449	2	US-09-679-397-2	Sequence 2, Appl
34	2029.5	84.6	449	2	US-09-680-148-2	Sequence 2, Appl
35	2029.5	84.6	449	2	US-09-304-465A-2	Sequence 2, Appl
36	2029.5	84.6	449	2	US-10-356-974-2	Sequence 2, Appl
37	2029.5	84.6	452	2	US-09-027-449-71	Sequence 71, Appl
38	2029.5	84.6	452	2	US-09-026-985-71	Sequence 71, Appl
39	2029.5	84.6	452	2	US-09-121-952A-71	Sequence 71, Appl
40	2029.5	84.6	452	2	US-09-234-340A-71	Sequence 71, Appl
41	2029.5	84.6	452	2	US-09-355-014-71	Sequence 71, Appl
42	2029.5	84.6	452	3	US-09-726-258-71	Sequence 71, Appl
43	2029	84.6	470	2	US-10-020-786-9	Sequence 9, Appl
44	2027.5	84.5	467	2	US-08-523-894-10	Sequence 10, Appl
45	2023	84.3	451	2	US-09-925-179-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

PCT-US96-13152-4  
Sequence 4, Application PC/TUS9613152

GENERAL INFORMATION:

APPLICANT: Martin, Ulrich, et al.

TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felfe & Lynch

ADDRESSEE: Attn: Norman D. Hanson

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Computer Disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/13152

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/578,953

FILING DATE: 27-Dec-95

APPLICATION NUMBER: EP 95 112 895.8

FILING DATE: 17-Aug-95

APPLICATION NUMBER: EP 95 114 969.9

FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:

NAME: Norman D. Hanson

REGISTRATION NUMBER: 30,946

REFERENCE/POCKET NUMBER: BOER 1059-PCT-PFF/NDH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 443

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-13152-4

Query Match 91.2%; Score 2189; DB 5; Length 443;  
Best Local Similarity 92.0%; Pred. No. 8.7e-161;

GenCore version 5.1.9  
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Cv protein - protein search, using sw model

Run on: June 6, 2006, 04:47:35 ; Search time 26.9954 Seconds  
(without alignments)  
1607.447 Million cell updates/sec

Title: US-10-724-274-31

Perfect score: 2399

Sequence: 1 EVOLVSGGLVQPGGSLRL.....MHEALHNHYTKSLSLGK 451

Sequence table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scored: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR\_80.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1743	72.7	327	1	G4HU		Ig gamma-4 chain C
2	1605.5	66.9	326	1	G2HU		Ig gamma-2 chain C
3	1590.5	66.3	330	1	GHU		Ig gamma-1 chain C
4	1585	66.1	377	2	A60764		Ig gamma-3 chain C
5	1575	65.7	377	2	A3511		Ig gamma-3 chain C
6	1524	63.5	470	2	S22080		Ig heavy chain pre
7	1479	61.7	472	2	S31459		Ig gamma-1 chain -
8	1466.5	61.1	444	2	PC4436		monoclonal antibod
9	1436.5	59.9	469	2	S37483		Ig gamma-2a chain
10	1431	59.6	446	2	S40295		Ig gamma-2a chain
11	1373	57.2	374	2	S63339		Ig heavy chain v
12	1344	56.0	474	1	G2MS11		Ig gamma-2b chain
13	1324.5	55.2	475	2	S01321		Ig gamma-2b chain
14	1289.5	53.8	328	2	I47159		Ig gamma 2a chain
15	1283.5	53.5	328	2	I47160		Ig gamma 2b chain
16	1264.5	52.7	328	2	I47161		Ig gamma 3 chain c
17	1240.5	51.7	328	2	I47158		Ig gamma 1 chain c
18	1199	50.0	323	1	GHRB		Ig gamma chain C r
19	1162	48.4	329	1	G2GP		Ig gamma-2 chain C
20	1147	47.8	308	2	C30554		Ig heavy chain C r
21	1139.5	47.5	255	4	S31866		Ig gamma-1 chain C
22	1129.5	47.1	234	2	P0207		Ig gamma chain C r
23	1124	46.9	333	2	PS0018		Ig gamma-2b chain
24	1118.5	46.6	326	2	PS0017		Ig gamma-1 chain c
25	1108.5	46.2	289	1	G3HUW1		Ig gamma-3 heavy c
26	1108	46.2	329	2	S00847		Ig gamma-2c chain
27	1106.5	46.1	324	1	G1MS		Ig gamma-1 chain C
28	1106.5	46.1	330	1	G2MSA		Ig gamma-2a chain
29	1103	46.0	327	2	S06611		Ig gamma-2 chain C

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004

C:Accession: A90933; A90249; A02150

R:Elison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30; 81-326 <PIN>

A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1, 111/1, 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (co light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Aen) #status predicted

Query Match	72.7%	Score	1743	DB	1	Length	327
Best Local Similarity	100.0%	Pred. No.	8.8e-94	Indels	0	Gaps	0
Matches	327	Conservative	0	Mismatches	0		
QY	125	ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAVLQSS	184				
Db	1	ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVSMNSGALTSGVHTFPAVLQSS	60				
QY	185	GLYSLSSVVTVFPSSSLGTNTYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPFELGGPSV	244				
Db	61	GLYSLSSVVTVFPSSSLGTNTYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPFELGGPSV	120				

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Gen protein - protein search, using sw model

on: June 6, 2006, 04:37:25 ; Search time 208.628 Seconds  
(without alignments)

1999.647 Million cell updates/sec

le: US-10-724-274-31

fect score: 2399

uence: 1 EQLVSGGLVQPGSLRL.....MHEALHHYTKSLSLGK 451

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 2849598 seqs, 925015592 residues

al number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

D: abase : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2041.5	85.1	469	2	Q569F4_HUMAN
2	2029	84.6	472	2	Q6N089_HUMAN
3	2022	84.3	478	2	Q6P181_HUMAN
4	2020	84.2	464	2	Q6M2U6_HUMAN
5	2016	84.0	470	2	Q6PJ44_HUMAN
6	2012.5	83.9	465	2	Q6P6C4_HUMAN
7	2009	83.7	473	2	Q8TC63_HUMAN
8	2008	83.7	466	2	Q6IN78_HUMAN
9	2003.5	83.5	473	2	Q6M2V7_HUMAN
10	2002.5	83.5	476	2	Q6M2X7_HUMAN
11	1987	82.8	470	2	Q7Z5W1_HUMAN
12	1985.5	82.8	544	2	Q6PJ95_HUMAN
13	1983	82.7	466	2	Q6N096_HUMAN
14	1979.5	82.5	475	2	Q6GMW7_HUMAN
15	1974.5	82.3	475	2	Q5EF85_HUMAN
16	1971.5	82.2	475	2	Q6M2O6_HUMAN
17	1963	81.8	480	2	Q6N094_HUMAN
18	1954	81.5	470	2	Q68CN4_HUMAN
19	1942.5	81.0	473	2	Q6P055_HUMAN
20	1937.5	80.8	521	2	Q8N4Y9_HUMAN
21	1934	80.6	482	2	Q7Z351_HUMAN
22	1923.5	80.2	481	2	Q6N097_HUMAN
23	1921	80.1	476	2	Q6GMX1_HUMAN
24	1918.5	80.0	465	2	Q6GMX6_HUMAN
25	1900.5	79.2	475	2	Q6N095_HUMAN
26	1898	78.9	518	2	Q6N030_HUMAN
27	1893	78.7	417	2	Q6N093_HUMAN
28	1897.5	78.7	519	2	Q5EBM2_HUMAN
29	1882	78.4	480	2	Q6PJF1_HUMAN
30	1872.5	78.1	475	2	Q5RE17_PONPY
31	1869.5	77.9	469	2	Q7Z7P5_HUMAN

32	1743	72.7	327	1	IGHG4_HUMAN	P01861	homo sapien
33	1669	69.6	348	2	IGHG1_HUMAN	Q6PVX1	homo sapien
34	1605.5	66.9	326	1	IGHG2_HUMAN	P01859	homo sapien
35	1590.5	66.3	330	1	IGHG1_HUMAN	P01857	homo sapien
36	1571	65.5	509	2	Q8NF17_HUMAN	Q8NF17	homo sapien
37	1551.5	64.7	467	2	Q4VBH1_RAT	Q4VBH1	rattus norv
38	1533.5	63.9	469	2	Q5M839_RAT	Q5M839	rattus norv
39	1519.5	63.3	465	2	Q510J0_RAT	Q510J0	rattus norv
40	1508	62.9	468	2	Q569B4_RAT	Q569B4	rattus norv
41	1506	62.8	470	2	Q4G060_RAT	Q4G060	rattus norv
42	1492	62.2	458	2	Q5M842_RAT	Q5M842	rattus norv
43	1486.5	62.0	461	2	Q5M7V3_RAT	Q5M7V3	homo sapien
44	1472	61.4	458	2	Q65ZQ1_HUMAN	Q65ZQ1	homo sapien
45	1470	61.3	354	2	Q86TT2_HUMAN	Q86TT2	homo sapien

#### ALIGNMENTS

##### RESULT 1

Q569F4\_HUMAN  
ID Q569F4\_HUMAN PRELIMINARY; PRT; 469 AA.  
AC Q569F4;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE IGHG1 protein.  
GN Name=IGHG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Buthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lymph;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RC TISSUE=Lymph;  
RG NIH MGC Project;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
CC EMBL; BC092518; AA92518.1; -; mRNA.  
CC SMR; Q569F4; 20-469.  
CC InterPro; IPR003599; Ig.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003597; Ig cl.  
CC InterPro; IPR003006; Ig\_MHC.  
CC InterPro; IPR003596; Ig\_v.